
WIRE RELEASE (TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 25 22:23:21 2000; MasPar time 35.62 Seconds
Tabular output not generated. 811.775 Million cell updates/sec

Title: >US-09-314-889-4
Description: (1-417) from US09314889.pep
Perfect Score: 3198
Sequence: 1 MEQRPRGCAVAAMALLVL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_plant 10:sp_plant 11:sp_todent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.427; Variance 85.811; scale 0.553

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3187	99.7	418	4	000275	LYMPHOCYTE ASSOCIATED	0.00e+00
2	2945	92.1	426	4	014865	DEATH RECEPTOR 3 BETA	0.00e+00
3	2483	77.6	380	4	000280	LYMPHOCYTE ASSOCIATED	0.00e+00
4	2451	76.6	372	4	000279	LYMPHOCYTE ASSOCIATED	0.00e+00
5	1577	49.3	253	4	000276	LYMPHOCYTE ASSOCIATED	0.00e+00
6	1423	44.5	277	4	014866	SOLUBLE DEATH RECEPTOR	2.10e-289
7	1329	41.6	234	4	000278	LYMPHOCYTE ASSOCIATED	1.37e-267
8	467	14.6	126	4	000277	LYMPHOCYTE ASSOCIATED	4.18e-72
9	272	8.5	471	6	019131	TUMOR NECROSIS FACTOR-	3.50e-31
10	228	7.1	616	4	09Y606	RECEPTOR ACTIVATOR OF	1.55e-22
11	218	6.8	327	6	09Y491	FAS PROTEIN.	1.27e-20
12	210	6.6	189	6	09Y530	TUMOR NECROSIS FACTOR	4.16e-19
13	212	6.6	625	11	035305	RECEPTOR ACTIVATOR OF	1.74e-19
14	206	6.4	189	6	09Y185	TUMOR NECROSIS FACTOR	2.35e-18
15	202	6.3	263	6	09X560	FAS ANTIGEN SPLICED VA	1.31e-17
16	202	6.3	320	6	09X529	C-TYPE FAS ANTIGEN.	1.31e-17
17	199	6.2	186	14	07Z735	SOLUBLE TNF RECEPTOR C	4.75e-17
18	198	6.2	186	14	09Y987	TUMOR NECROSIS FACTOR	4.75e-17
19	199	6.2	316	14	057092	TUMOR NECROSIS FACTOR	3.99e-16
20	194	6.1	186	14	09WJ84	TUMOR NECROSIS FACTOR	3.99e-16

21	193	6.0	283	6	09X528	HVEAS.	6.10e-16
22	193	6.0	283	4	09Z956	HERPESVIRUS ENTRY MEDI	6.10e-16
23	190	5.9	314	4	014293	FAS SOLUBLE PROTEIN.	2.17e-15
24	187	5.8	320	14	057300	TUMOR NECROSIS FACTOR	7.66e-15
25	187	5.8	320	14	057091	TUMOR NECROSIS FACTOR	7.66e-15
26	187	5.8	322	14	072761	K2R PROTEIN.	7.66e-15
27	178	5.6	348	14	057112	TUMOR NECROSIS FACTOR	3.24e-13
28	178	5.6	348	14	085407	HOMOLOG OF VACCINIA VI	3.24e-13
29	180	5.6	349	14	057109	TUMOR NECROSIS FACTOR	1.42e-13
30	179	5.6	349	14	085118	SOMALIA-1977 RIGHT NEA	2.15e-13
31	179	5.6	349	14	057111	TUMOR NECROSIS FACTOR	2.15e-13
32	179	5.6	349	14	057110	TUMOR NECROSIS FACTOR	2.15e-13
33	179	5.6	349	14	089098	GARCIA-1966 RIGHT NEAR	2.15e-13
34	175	5.5	350	14	057116	TUMOR NECROSIS FACTOR	1.68e-12
35	174	5.4	348	14	057103	TUMOR NECROSIS FACTOR	1.68e-12
36	174	5.4	348	14	057108	TUMOR NECROSIS FACTOR	1.68e-12
37	174	5.4	348	14	057277	TUMOR NECROSIS FACTOR	1.68e-12
38	174	5.4	349	14	057098	TUMOR NECROSIS FACTOR	1.68e-12
39	174	5.4	349	14	057099	TUMOR NECROSIS FACTOR	1.68e-12
40	174	5.4	349	14	057291	TUMOR NECROSIS FACTOR	1.68e-12
41	174	5.4	349	14	057102	TUMOR NECROSIS FACTOR	1.68e-12
42	174	5.4	349	14	057101	TUMOR NECROSIS FACTOR	1.68e-12
43	174	5.4	349	14	057100	TUMOR NECROSIS FACTOR	1.68e-12
44	174	5.4	349	14	057284	TUMOR NECROSIS FACTOR	1.68e-12
45	174	5.4	355	14	085308	SECRETED RECEPTOR BIND	1.68e-12

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	418 AA.
ID	000275			
AC	000275;			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97272273.			
RA	SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,			
RA	MCMICHAEL A.J., BELL J.I.;			
RT	"LARD: a new lymphoid-specific death domain containing receptor			
RT	regulated by alternative pre-mRNA splicing."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).			
DR	EMBL: U94502; AAC51307.1; "			
DR	HSSP: P19438; 1TNR.			
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.			
DR	PFAM: PF00531; death; 1.			
DR	PFAM: PF00020; TNFR_c6; 2.			
SQ	SEQUENCE 418 AA; 45456 MW; 3D04954A CRC32;			
Query Match	99.7%;	Score 3187;	DB 4;	Length 418;
Best Local Similarity	99.8%;	Pred. No. 0.00e+00;		
Matches	417;	Conservative	0;	Mismatches 0; Indels 1; Gaps 1
Db	1	MEQRPRGCAVAAMALLVLICARAGGTRSPRCDCAGFHKKIGIFCCRCGPAHYLAP	60	
Qy	1	MEQRPRGCAVAAMALLVLICARAGGTRSPRCDCAGFHKKIGIFCCRCGPAHYLAP	60	
Db	61	CTEPCGNTSLVPCQDFFLAMENHNHNSCARCQACDEQASOVALENCASAVADTRCGCKPG	120	
Qy	61	CTEPCGNTSLVPCQDFFLAMENHNHNSCARCQACDEQASOVALENCASAVADTRCGCKPG	120	
Db	121	WFEVCQVSSQCVSSPFCQPCDGLGALHRRHRLCSRRDTCGTLPGFYEHGDCVSCP	180	
Qy	121	WFEVCQVSSQCVSSPFCQPCDGLGALHRRHRLCSRRDTCGTLPGFYEHGDCVSCP	180	
Db	181	TSTIGSCPERRCAACGMRQWVQVLLAGLVVPLLLGATITTYTHRCMPHKLPLVAADEA	240	
Qy	181	TSTIGSCPERRCAACGMRQWVQVLLAGLVVPLLLGATITTYTHRCMPHKLPLVAADEA	240	

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DB 241 GNEALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOALCPQVWTS 300
OY 240 GNEALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOALCPQVWTS 299
DB 301 WQOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFVTLGLREA 360
OY 300 WQOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFVTLGLREA 359
DB 361 IEAVEVEIGFRFDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLSRLQGRP 418
OY 360 IEAVEVEIGFRFDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLSRLQGRP 417

RESULT 2
ID 014865 PRELIMINARY; PRT: 426 AA.
AC 014865
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE DEATH RECEPTOR 3 BETA.
GN DR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98113360.
RA MARZOCCHA K., RIBEIRO P., CHARLOT C., RENARD N., COFFIER B.,
RA SALLES G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas."
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
RL EMBL: AF026070; AAC39556.1; -.
RL HSSP: P19438; ITNR.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PFAM: PF00531; death; 1.
DR PFAM: PF00020; TNFR_C6; 2.
SQ SEQUENCE 426 AA; 45950 MW; 87E0821 CRC32;

Query Match 92.1%; Score 2945; DB 4; Length 426;
Best Local Similarity 94.1%; Pred. No. 0.00e+00;
Matches 401; Conservative 8; Mismatches 8; Indels 9; Gaps 5;

DB 1 MEORPRGCAAAVAAALLVLLGARAAGSTRSPRCDCAGDFHKKTIGLFCRCGCPAGHYLKAP 60
OY 1 MEORPRGCAAAVAAALLVLLGARAAGSTRSPRCDCAGDFHKKTIGLFCRCGCPAGHYLKAP 60
DB 61 CTEPCGNSCTLVCPQDTFLAMENHNHNSCARQACDQASQVVALENCASVADTRCGCKPG 120
OY 61 CTEPCGNSCTLVCPQDTFLAMENHNHNSCARQACDQASQVVALENCASVADTRCGCKPG 120
DB 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
OY 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
DB 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
OY 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
DB 181 TPPLSLAGPAGVAVSLVAGGAGVFWVQVLLAGLVPLLGATLTYTYRHQWPKR 240
OY 181 TPPLSLAGPAGVAVSLVAGGAGVFWVQVLLAGLVPLLGATLTYTYRHQWPKR 240
DB 181 TS--TLGSCP--E--RCA--AVCGMR--QMFVWVLLAGLVPLLGATLTYTYRHQWPKR 231
OY 181 TS--TLGSCP--E--RCA--AVCGMR--QMFVWVLLAGLVPLLGATLTYTYRHQWPKR 231
DB 241 PLVVADEAGMALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOAL 300
OY 241 PLVVADEAGMALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOAL 291
DB 232 PLVVADEAGMALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOAL 291
OY 232 PLVVADEAGMALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOAL 291
DB 301 LCPQVWMTDOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFV 360
OY 292 LCPQVWMTDOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFV 351
DB 361 RTTGLREAEIEAVEVEIGLFRDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLS 420
OY 352 RTTGLREAEIEAVEVEIGLFRDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLS 411
DB 421 RLQGRP 426

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OY 412 RLQGRP 417

RESULT 3
ID 000280 PRELIMINARY; PRT: 380 AA.
AC 000280;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97272273.
RA SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
RA MCMICHAEL A.J., BELL J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RL EMBL: U94510; AAC51315.1; -.
RL HSSP: P19438; ITNR.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PFAM: PF00531; death; 1.
DR PFAM: PF00020; TNFR_C6; 2.
SQ SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;

Query Match 77.6%; Score 2483; DB 4; Length 380;
Best Local Similarity 90.9%; Pred. No. 0.00e+00;
Matches 379; Conservative 1; Mismatches 0; Indels 37; Gaps 1;

DB 1 MEORPRGCAAAVAAALLVLLGARAAGSTRSPRCDCAGDFHKKTIGLFCRCGCPAGHYLKAP 60
OY 1 MEORPRGCAAAVAAALLVLLGARAAGSTRSPRCDCAGDFHKKTIGLFCRCGCPAGHYLKAP 60
DB 61 CTEPCGNSCTLVCPQDTFLAMENHNHNSCARQACDQASQVVALENCASVADTRCGCKPG 120
OY 61 CTEPCGNSCTLVCPQDTFLAMENHNHNSCARQACDQASQVVALENCASVADTRCGCKPG 120
DB 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
OY 121 WFEVCQVQCVCSSSPFYCQPCLDGALHRTLLCSRRDTCGTLPGFEHGDGCVSCP 180
DB 181 TPPLSLAGPAGVAVSLVAGGAGVFWVQVLLAGLVPLLGATLTYTYRHQWPKR 240
OY 181 TPPLSLAGPAGVAVSLVAGGAGVFWVQVLLAGLVPLLGATLTYTYRHQWPKR 240
DB 204 MEALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOALCPQVWTS 263
OY 241 MEALTPPETHLSPDLSAHTLLAPPDSSEKICTVOLVGNWMTGYPETOALCPQVWTS 300
DB 264 DOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFVTLGLREA 323
OY 301 DOLPSRALGPAAAPTLSPSPAGSPAMMLOPGPOLYDVMDAVPARMKKEFVTLGLREA 360
DB 324 IEAVEVEIGFRFDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLSRLQGRP 380
OY 361 IEAVEVEIGFRFDOOYEMLKRMRQOOPAGLCAVVALEFRMGIDGCVEDLSRLQGRP 417

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RESULT 4
ID 000279 PRELIMINARY; PRT: 372 AA.
AC 000279;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 8.
DE (LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

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RN [1]
 RP SEQUENCE FROM N.A.
 RA SCREATION G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,
 RA BELL J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U94509; AAC51314.1; -;
 DR EMBL: U94506; AAC51311.1; -;
 DR HSSP: P19438; 1TNR.
 DR PFAM: PF00531; death; 1.
 KW Alternative splicing.
 SQ SEQUENCE 372 AA; 40391 MW; 430DA0D5 CRC32.

Query Match	76.68;	Score 2451;	DB 4;	Length 372;
Best Local Similarity	98.58;	Pred. No. 0.00e+00;		
Matches 321;	Conservative 2;	Mismatches 2;	Indels 1;	Caps 1;

Db	48	CRGPA - ASOVALENCASAVADTRCGCKRGMFVEQVQCVSSSPFCQPCDLCGALHRT	106
Qy	92	CQACDEQASOVALENCASAVADTRCGCKRGMFVEQVQCVSSSPFCQPCDLCGALHRT	151
Db	107	RLCSRRDTRDGTCLPFGFEHGDGCVSCPNTSLGSCPERCAAVCGMRQMFVWVLLAGLV	166
Qy	152	RLCSRRDTRDGTCLPFGFEHGDGCVSCPNTSLGSCPERCAAVCGMRQMFVWVLLAGLV	211
Db	167	VPLLIGATLTYTTHCHCMPHKPLVTADAGAEALTPPATHLSPDLSAHTLLAPDSSEKI	226
Qy	212	VPLLIGATLTYTTHCHCMPHKPLVTADAGAEALTPPATHLSPDLSAHTLLAPDSSEKI	271
Db	227	CTVOLGNSWTPGYETFOEALCPQVTVMSDQLPSRALGPAAAPTLSPESPAGSPAMLOP	286
Qy	272	CTVOLGNSWTPGYETFOEALCPQVTVMSDQLPSRALGPAAAPTLSPESPAGSPAMLOP	331
Db	287	GPQLYDWDVAVPARRKMEFYRTGLRBAELIENAVEVEIGRRDDOQYEMLKRWROQDPAGIG	346
Qy	332	GPQLYDWDVAVPARRKMEFYRTGLRBAELIENAVEVEIGRRDDOQYEMLKRWROQDPAGIG	391
Db	347	AVYAALERMGLDGCVEDLRSRLQGP	372
Qy	392	AVYAALERMGLDGCVEDLRSRLQGP	417

RESULT	5		
ID	000276	PRELIMINARY;	PRT; 253 AA.
AC	000276;		
DT	01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Primates; Carnivora; Catarrhini; Homiidae; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 97272273.		
RA	SCHEAFAN G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,		
RA	MCMICHAEL A.J., BELL J.I.;		
RT	"LARD: a new lymphoid-specific death domain containing receptor		
RT	regulated by alternative pre-mRNA splicing."		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).		
DR	EMBL; U94503; AAC51308.1; -		
DR	HSSP; P19438; 1TNR.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.		
DR	PFAM; PF00020; TNFR_Cat_2.		
SQ	SEQUENCE 253 AA; 26934 MW; A210CB63E CRC32;		

Query Match	49.3%	Score 1577	DB 4	length 253
Best Local Similarity	99.0%	Pred. No.	0	00+00
Matches	200	Conservative	0	Mismatches 2; Indels 0; Gaps 0;
Db	1	MEORPRCGAAVAAALLLVLLGARGAGCTRSFRCDACADPFHKITGLFCRCRCPAGHYTKAP	60	
	1	MEORPRCGAAVAAALLLVLLGARGAGCTRSFRCDACADPFHKITGLFCRCRCPAGHYTKAP	60	

Db	61	CTEPGNTCTLCVQDPDPLAENHNHNSBCARQACQACDEQASQVALENCSAIVADTRCGCKPg	120
Qy	61	CTEPGNTCTLCVQDPDPLAENHNHNSBCARQACQACDEQASQVALENCSAIVADTRCGCKPg	120
Db	121	MFVEQVSQCVSSSPFCQPCPLDGCALHRIHRIILCSRRDIDCGTLPGFEHHDGCVSCP	180
Qy	121	MFVEQVSQCVSSSPFCQPCPLDGCALHRIHRIILCSRRDIDCGTLPGFEHHDGCVSCP	180
Db	181	TSTLGSCEPERCAAVCGNRQRM 202	
Qy	181	TSTLGSCEPERCAAVCGNRQRM 202	

RESULT	6
ID	014866
PRELIMINARY;	
PRT;	277 AA.

DT 01-JAN-1998 (TREMBLrel) 05, Created
 DT 01-JAN-1998 (TREMBLrel) 05, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel) 12, Last annotation update)
 DE SOLUBLE DEATH RECEPTOR 3 BETA.
 GN DR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MARZOCCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
 RA SALES G.;
 RL submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026071; AAB82288.1; -.
 DR HSSP: P19438; ITNR.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PFWAM: PF00020; TNFR_c6; 2.
 DQ SEQUENCE 277 AA; 29111 MW; 06E165C7 CRC32.

Query Match	44.5%;	Score 1423;	DB 4;	Length 277;
Best Local Similarity	99.5%;	Pred. No. 2.10e-289;		
Matches	181;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Db	1	MEPRRGCAAAVAAALLLVLLGARAAGGSTRSPRCACADPFHKTGLPCCRCPAGHYLKAP	60
OY	1	MEQRRGCAAAVAAALLLVLLGARAAGGSTRSPRCACADPFHKTGLPCCRCPAGHYLKAP	60
Db	61	CTEPGNGSTCLVCPQDPTFLAMENHNHNSRCACQACDEQASQVALENCNSAADPTRCGCKPG	120
OY	61	CTEPGNGSTCLVCPQDPTFLAMENHNHNSRCACQACDEQASQVALENCNSAADPTRCGCKPG	120
Db	121	WFVECVSQCVSSSPFFTCQPLDCGALHNRHTRLICSSRRDTCGTCLPGFYEHGDCVSCP	180
OY	121	WFVECVSQCVSSSPFFTCQPLDCGALHNRHTRLICSSRRDTCGTCLPGFYEHGDCVSCP	180
Db	181	TP 182	
OY	181	TS 182	

RESULT	7	PRELIMINARY:	PRT:	234	AA.
ID	000278:				
AC	000278:				
DT	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)				
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)				
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 7.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Carnivora; Hominiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 97272273.				
RX	MEGLIN G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,				
RA	MICHAEL A.J., BELL J.I.:				
RT	"LARD: a new lymphoid-specific death domain containing receptor				
RT	regulated by alternative pre-mRNA splicing.";				

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RL  PROC. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR  EMBL; U94508; AAC51313.1; -.
DR  PFAM; PF00531; death; 1.
SQ  SEQUENCE 234 AA; 25373 MW; 272FD3C9 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1,37e-267;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  ADEGMALPPPAHSHLAPDPSSEKICVQVGNWPTGPTOTALCPQ 112
    |||
QY  ADEGMALPPPAHSHLAPDPSSEKICVQVGNWPTGPTOTALCPQ 295
    |||
Db  113 VTMWMDLPSPRALPAAAPTLSPESPAGSPAMMLQPGFQLYDMDVAPARRKKEFVRTLG 172
    |||
QY  VTMWMDLPSPRALPAAAPTLSPESPAGSPAMMLQPGFQLYDMDVAPARRKKEFVRTLG 355
    |||
-Db  173 LREAIEAVEVEIGRFROQYEMLKRMOQOPAGIGAYVAALERMGLDGCVEDLRSRLOR 232
    |||
QY  LREAIEAVEVEIGRFROQYEMLKRMOQOPAGIGAYVAALERMGLDGCVEDLRSRLOR 415
    |||
Db  233 GP 234
    ||
QY  416 GP 417

RESULT 8
ID 000277; PRELIMINARY; PRT; 126 AA.
AC 000277;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE LYMPOCYTE ASSOCIATED RECEPTOR OF DEATH 6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97272273.
RA SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
RA MICHAEL A.J., BELL J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94507; AAC51312.1; -.
SQ SEQUENCE 126 AA; 13349 MW; B4B4851A CRC32;

Query Match
Best Local Similarity 92.2%; Pred. No. 4.18e-72;
Matches 59; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Db  48 CRGCPA-ASOVALENCASVADTRCGCKGWFVECOVSQCVSSSPFYCOPCLDGLHRRHT 106
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QY  92 CQACDEQASOVALENCASVADTRCGCKGWFVECOVSQCVSSSPFYCOPCLDGLHRRHT 151
    |||
Db  107 RLIC 110
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QY  152 RLIC 155

RESULT 9
ID 019131; PRELIMINARY; PRT; 471 AA.
AC 019131;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TUMOR NECROSIS FACTOR-RECEPTOR I.
GN TNF-RI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-AORTA;
RA LEE E.-K., TAYLOR M.J., KEHRLI M.E.;
RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90937; AAB65143.1; -.
DR HSSP; P19438; 1TNR.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PFAM; PF00531; death; 1.
DR PFAM; PF00020; TNFR_C6; 3.
SQ SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;

Query Match
Best Local Similarity 30.0%; Pred. No. 3.50e-31;
Matches 128; Conservative 79; Mismatches 169; Indels 51; Gaps 34;

Db  40 RESPCP-QGKYNHPONSTICCTCHGKTYLYNDPCPGRTDRCVAPGTYTLENHRLR 98
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QY  29 RSFRCCAGDF-HKKYGLFCRCRCPPAGHYLKAPCTPCGNSSTLCVCPDFTLMMHNHS 87
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Db  99 -CLSCRCDEMPQVEISPCVVDRTVCGCRKQRYREYV-GE-TGFRCLNCSLCPN-GTV 154
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QY  88 ECARGCACEQASOVALENCASVADTRCGCKGWFVECOVSQCVSSSPFYCOPCLDGLAL 147
    |||
Db  155 NIPCO--ERDPTIC-HCHMGFFLKAKCISCHDKNKECEKLPPTSTGKSDOPGTT 210
    |||
QY  148 HRHRLCRRDPDCCGTCPLGFYEHGDGVCSTPLGSCPERCAA-VC-GW-RQHFVWQ 204
    |||
Db  211 VLLPLVYFGCLASAVYVLAACRYQWRKPKLYSIICGOSTLYKGEPELIVAPGFNP 270
    |||
QY  205 VLLAGLVV-PL-LLG-ATLTYYR-HCWPHK--PLV---T-ADEGMALTP-P--PA 249
    |||
Db  271 TWCFSSSTPSSPVSIPIYISCDNSNFGAVASPSSTAPPHLKAGILPQPASTHLCTP 330
    |||
QY  250 THL--SPDLSATHLAP--DSSK--ICTVOLGNWPTGPTOTALC-PQYTWGSD-DQ 302
    |||
Db  331 GPPASTHLCTPQPASTHLCTPYQKWEASAPSDQLADAPATLYAVYDGVPPSRKEL 390
    |||
QY  303 -LPSRA-L--GPAAPTL-SP---ESPA-GSPAMMLQPGP-LYDMDVAPARRKKEF 350
    |||
Db  391 VRLIGSEHEIRLEENRHLREAOYSMLAMRRTPPREATLELLGRLRMDLGL 450
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QY  351 VRLIGREIEAVEVEIGR-FRDOQYEMLKRMOQOP--AGLAVYVAALERMGLDGC 406
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Db  451 ENIEEAL 457
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QY  407 EDLRSRL 413

RESULT 10
ID 09Y606; PRELIMINARY; PRT; 616 AA.
AC 09Y606;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECEPTOR ACTIVATOR OF NUCLEAR FACTOR-KAPPA B.
GN RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98032977.
RA ANDERSON D.M., MARASKOVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,
RA TOMETSKO M.E., ROUX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,
RA GALIBERT L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function."
RL Nature 390:175-179(1997).
DR EMBL; AF018253; AAB86809.1; -.
KW Receptor.
SQ SEQUENCE 616 AA; 66033 MW; 6AF398F8 CRC32;

Query Match
7.1%; Score 228; DB 4; Length 616;

```


OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.

RN [1]

RP SEQUENCE FROM N.A.

RA DUTHIE S., NASIR L., ECKERSALL P.D.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; U72344; AAB95089.1; -.

DR HSSP; P19438; 1EXT.

DR PROSITE; PS00652; TMR_NGFR_1; 3.

DR PFAM; PF00020; TMR_C6; 3.

FT NON TER

SO SEQUENCE 189 AA; 21420 MW; 687732D2 CRC32;

Query Match

6.4%; Score 206; DB 6; Length 189;

Best Local Similarity 31.8%; Pred. No. 2.35e-18;

Matches 49; Conservative 24; Mismatches 67; Indels 14; Gaps 11;

Db 40 RAIPCP-OGKXIHPODNSICCKHKGITLYNDCEPGGLDTCRCGENTFTASENYLR- 97

QY 29 RSPRCDCAGDF-HKRIGLFCRCGCPAGHYLAKPCTEPCGNSSTCLVCPDPTFLAMENHNS 87

Db 98 QCLSCSKCKEMGYEISPCYVYRDTVCGCRK---N-QY-RYVSETHF-Q-CLNCSIC 149

QY 88 ECARQACDEQASVALENCASAVADTRCGCKPGWFEQVSOQVSSPFYCPCLDCGA- 146

Db 150 LNTVQISCKETQNTVC-TCHAGFFLRGNECVSC 182

QY 147 LHRHTRLCS--RRDTCGCTCLPGFEHGDGCVSC 179

RESULT 15

ID 09XS60 PRELIMINARY; PRT; 263 AA.

AC 09XS60;

DT 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)

DE FAS ANTIGEN SPLICED VARIANT.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.

RN [1]

RP SEQUENCE FROM N.A.

RA ISONO T., TANBE Y., NAGANO Y., SETO A.;

RT "Splicing and allelic variation in the rabbit Fas antigen gene.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB021297; BAA78429.1; -.

SO SEQUENCE 263 AA; 30374 MW; 43BF129F CRC32;

Query Match

6.3%; Score 202; DB 6; Length 263;

Best Local Similarity 34.0%; Pred. No. 1.31e-17;

Matches 32; Conservative 19; Mismatches 37; Indels 6; Gaps 5;

Db 41 GNFCQQLCPPTGKKKADCTSNKGKPCDCEPCEGEFTD-KSHPSKCRCSLCDGEGHLE 99

QY 44 GLFCRCGCPAGHYLAKPCTEPCGNSSTCLVCPDPTFLAMENHNSCARQACD-EQASQ 101

Db 100 VETD-CTTIQNTKCRCKSNF--CNALKECHDP 130

QY 102 VALENCASAVADTRCGCKPGWFEQVSOQVSSSP 135

Search completed: Tue Jul 25 22:23:58 2000

Job time : 37 secs.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 06:03:21 ; Search time 1177.05 Seconds
(without alignments)
1901.371 Million cell updates/sec

Title: US-09-314-889-3
Perfect score: 1254
Sequence: 1 ATGGAGCAGCGCGCGCGGGG.....GCCCTGCAGCGCGCGCGCTGA 1254

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pl1: *
10: gb_pl2: *
11: gb_pl3: *
12: gb_ro: *
13: gb_sts: *
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16: em_fun: *
17: em_hum1: *
18: em_hum2: *
19: em_in: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_sy: *
29: em_un: *
30: em_v1: *
31: gb_htg1: *
32: gb_htg2: *
33: gb_in1: *
34: gb_in2: *
35: em_ba1: *
36: em_ba2: *
37: em_hum3: *
38: em_hum4: *
39: gb_pr4: *
40: gb_htg3: *
41: gb_htg4: *
42: gb_htg5: *
43: gb_htg6: *

44: gb_htg7: *
45: em_htg1: *
46: em_htg2: *
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49: gb_pl3: *
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79: gb_htg30: *
80: gb_htg31: *
81: gb_v11: *
82: gb_v12: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1254	100.0	1254	11	HSU72763	U72763 Human death
2	1254	100.0	1254	11	HSU78029	U78029 Human apopto
3	1254	100.0	1254	11	HSU94501	U94501 Human lymph
4	1254	100.0	1634	11	HSU74611	U74611 Human Apo-3
5	1241	99.0	1257	11	HSU94502	U94502 Human lymph
6	1234.8	98.5	1528	11	HSU83597	U83597 Human death
7	1233.8	98.4	1557	11	HSU75380	U75380 Human apopto
8	1197.4	95.5	1669	11	AF026070	AF026070 Homo sapi
9	1143	91.1	1355	11	HSU94503	U94503 Human lymph
10	1133.4	90.4	1743	9	HSW61	Y09392 H.sapiens m
11	1132	90.3	1198	11	HSU94504	U94504 Human lymph
12	1103.4	88.0	1763	11	AF026071	AF026071 Homo sapi
13	1022	81.5	1143	11	HSU94510	U94510 Human lymph
14	974	77.7	1119	11	HSU94509	U94509 Human lymph
15	910	72.6	1087	11	HSU94505	U94505 Human lymph
16	630	50.2	952	11	HSU94506	U94506 Human lymph
17	547.8	43.7	705	11	HSU94508	U94508 Human lymph
18	535.4	42.7	809	11	HSU94512	U94512 Human lymph
19	527.4	42.1	816	11	HSU83598	U83598 Human death
20	526.4	42.0	808	11	HSU75381	U75381 Human apopto
21	510.4	40.7	838	11	HSU94507	U94507 Human lymph
22	342.2	27.3	651	11	HSU83599	U83599 Human alter
23	331.4	26.4	121345	40	AL158217	AL158217 Homo sapi
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ALIGNMENTS

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					Gaps
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QY	61	GGGGCCCCGGGCGCCAGGGCGGCACTGCTACGCCAGGTGACGTGTGCGGTACTTCCAC	120		
Db	61	GGGGCCCCGGGCGCCAGGGCGGCACTGCTACGCCAGGTGACGTGTGCGGTACTTCCAC	120		
QY	121	AAGAAGATTGTGTTGTTTTTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCC	180		
Db	121	AAGAAGATTGTGTTTTTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCC	180		
QY	181	TGCACGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCAAGACACTTCTTGGCC	240		
Db	181	TGCACGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCAAGACACTTCTTGGCC	240		
QY	241	TGGAGAACCAACATATTGTGAATGTGCCCGCGTGCACGCTGTGATGAGAGGCGTCC	300		
Db	241	TGGAGAACCAACATATTGTGAATGTGCCCGCGTGCACGCTGTGATGAGAGGCGTCC	300		
QY	301	CAGGTGCGCTGGAGAACTGTTCAGCAGTGGCGCACCCGCGTGTGCTGTAAAGCAGGC	360		
Db	301	CAGGTGCGCTGGAGAACTGTTCAGCAGTGGCGCACCCGCGTGTGCTGTAAAGCAGGC	360		
QY	361	TGGTTTGTGAGATGCGCAGGTGACGCAATGTGTACAGATTCACCTGTACTGCGCAACA	420		
Db	361	TGGTTTGTGAGATGCGCAGGTGACGCAATGTGTACAGATTCACCTGTACTGCGCAACA	420		
QY	421	TGCTTAGACTGCGGGGGCCCTGCACCGCCCAACACGGCTCTCTGTTCGCGAGAGATCT	480		
Db	421	TGCTTAGACTGCGGGGGCCCTGCACCGCCCAACACGGCTCTCTGTTCGCGAGAGATCT	480		
QY	481	GACTGTGGGACCTGCTGCTGCTGCTTCTATGAACATGCGGATGCGTGTCTGTGCCCC	540		
Db	481	GACTGTGGGACCTGCTGCTGCTGCTTCTATGAACATGCGGATGCGTGTCTGTGCCCC	540		
QY	541	ACGAGCACCCCTGGGGAGCTCTCCAGAGCGCTGCGCGTGTGTGGCGGAGAGCATG	600		
Db	541	ACGAGCACCCCTGGGGAGCTCTCCAGAGCGCTGCGCGTGTGTGGCGGAGAGCATG	600		
QY	601	TTCTGGGTCCAGGTGCTCTGCGCTGTGTGTGTCCTCTCTGTGGGCGCACCTG	660		
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QY	661	ACCTACACATACCGCACCTGTGGGCTGCACAAACCCCTGGTTACGTACGATACATCTGG	720		
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QY	721	ATGAGAGCTGTGACCCCAACACCGGCGCACCATCTGTCAACCTTGGACGCGCCACAC	780		
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QY	781	CTTCTACACCTCTCTGACACACATGAGAAATGTGCACCCGTCCAGTGTGGGTAAACGC	840		
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QY	841	TGACACCCCTGGATACCCCGAGACCCAGAGAGGCTGTGCCCGCAGGTGACATGTCTGG	900		
Db	841	TGACACCCCTGGATACCCCGAGACCCAGAGAGGCTGTGCCCGCAGGTGACATGTCTGG	900		
QY	901	GACCAATTGCCCCACAGAGCTTTTGGCCCGCGTGTGCGGCACACCTCTGCGCAGAGTCC	960		
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 DB 1021 GGGGTCACAGCGGGCGCTGGAAGAGATTGTCGGCAGCGTGGGGGTGCGCGAGAG 1080
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 DB 1141 CGCTGGCGCCAGCAGAGCCCGGGGCGTCGGAGCGGCTTACCGGGGCGCTGAGCGCATG 1200
 OY 1201 GGGGCTGAGAGCGCTGGCTGGAGAGATTGGCAGCGCGCTGAGCGCGCCGTGA 1254
 DB 1201 GGGGCTGAGAGCGCTGGCTGGAGAGATTGGCAGCGCGCTGAGCGCGCCGTGA 1254
 RESULT 2
 HSU78029 1254 bp mRNA PRI 15-JAN-1997
 LOCUS Human apoptosis inducing receptor AIR mRNA, complete cds.
 DEFINITION U78029
 ACCESSION U78029.1 GI:1778763
 VERSION 1
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1254)
 Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and
 Goodwin, R.G.
 AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
 of Apoptosis
 Unpublished
 2 (bases 1 to 1254)
 Degli-Esposti, M.A. and Goodwin, R.G.
 Direct Submission
 Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
 University Street, Seattle, WA 98101, USA
 FEATURES
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 TLVTYRHCMHDKPLVTADEAGMEALTPRPALHSLPSLSAHTLLAPPSSEKTVOL
 VGNMTGPETFOALCPQYVWMSDQLPSRALGPRAAATPLSPESAGSPAMHLOPQPO
 LYDMADVPAHRMKEFYNTLDUREAIEAIVEIGRFDDQTEMLKRWKQDPAGIGA
 VYALERNGDGCVEEDLSRLQRRP"
 BASE COUNT 201 a 420 c 407 g 226 t
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 Query Match 100.0%; Score 1254; DB 11; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 2.4e-204;
 Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 841 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTGTGCCGAGGTGACATGTGCTCGG 900
 OY 901 GACCAGTTGGCCAGCAAGCTGTTGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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QY	1201	GGGCTGGAGCGGTGCTGGAGAAGACTTGCCGACGCCCTTCAGCGGCCCCGTGA	1254
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RESULT	3		
LOCUS	HSU94501		
DEFINITION	Human lymphocyte associated receptor of death 1a mRNA, complete cds.		
ACCESSION	U94501		
VERSION	U94501.1		
KEYWORDS	GI:2071948		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1254) Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.T.		
TITLE	LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)		
JOURNAL	97272273		
MEDLINE	2 (bases 1 to 1254)		
REFERENCE	Screation,G.R.		
AUTHORS	Direct Submission		
TITLE	Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK		
JOURNAL			
FEATURES	source		
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QY	61	GGGGCCCGGGCCCAAGGGGGGCACTGTAAGCCCAGAGTGTGACTGTGCCGTACTTCCAC	120
Db	61	GGGGCCCGGGCCCAAGGGGGGCACTGTAAGCCCAGAGTGTGACTGTGCCGTACTTCCAC	120
QY	121	AAGAAGATTGGTCTTTTGTGGCAGAGAGCTGCCACAGGGGGCACTACTGAAGCCCT	180
Db	121	AAGAAGATTGGTCTTTTGTGGCAGAGAGCTGCCACAGGGGGCACTACTGAAGCCCT	180

OY	181	TGACGAGCCCTCGGCAACATCCACTGCGTGTGTGTGTCCCAAGACACTTTTGGCC	240
Db	181	TGCACGGAGCCCTCGGCAACTCCACTGCTTGTGTGTGTCCCAAGACACTTTTGGCC	240
OY	241	TGGGAGAACCAACCAATTAATTCATGATGTGCCCGCTGGCAGAGCCGTGTATGAGCAGGCCTCC	300
Db	241	TGGGAGAACCAACCAATTAATTCATGATGTGCCCGCTGGCAGAGCCGTGTATGAGCAGGCCTCC	300
OY	301	CAGGTGGCGCTGGAGAACCTGTCACGACGTGGCCAGACCCCGCTGTGGCTGTAAAGCCAGGC	360
Db	301	CAGGTGGCGCTGGAGAACCTGTCAGCGAGTGTGGCCAGACCCCGCTGTGGCTGTAAAGCCAGGC	360
OY	361	TGGTTTGTGGATGTCCAGAGTCCAGAGTCCAAATGTGTAGAGATTCAACCTTTTACTGTCCACCA	420
Db	361	TGGTTTGTGGATGTCCAGAGTCCAGAGTCCAAATGTGTAGAGATTCAACCTTTTACTGTCCACCA	420
OY	421	TGCGTAGACTCGGGGGCCCTGCAACCGCCACACAGGCTACTCTGTTCCTCCGACAGATACT	480
Db	421	TGCGTAGACTCGGGGGCCCTGCAACCGCCACACAGGCTACTCTGTTCCTCCGACAGATACT	480
OY	481	GACTGTGGGACCTTCCCTTGGCTTCTATGAACATGTGGGATGTGGCTGTGTCTGTGCCCC	540
Db	481	GACTGTGGGACCTTCCCTTGGCTTCTATGAACATGTGGGATGTGGCTGTGTCTGTGCCCC	540
OY	541	ACGAGACCCCTGGGGAGCTCTCCAGAGACCGCTGTGCCGTGTGTGTGGCTGTGAGAGCAGATG	600
Db	541	ACGAGACCCCTGGGGAGCTCTCCAGAGACCGCTGTGCCGTGTGTGTGGCTGTGAGAGCAGATG	600
OY	601	TTTCTGGGTCCAGAGTGTCTCTGTGGCTTGTGTGTGTCCCTCTGTGTGGGGCCACCCGTG	660
Db	601	TTTCTGGGTCCAGAGTGTCTCTGTGGCTTGTGTGTGTGTCCCTCTGTGTGGGGCCACCCGTG	660
OY	661	ACCTACACATATCCGCGCACTGTGGGCTTCACAAACCCCTGTGTACTGTCAATGAATCAACTGG	720
Db	661	ACCTACACATATCCGCGCACTGTGGCTTCACAAACCCCTGTGTACTGTCAATGAATCAACTGG	720
OY	721	ATGAGAGCTCTGACCCCAACCAACGGGCCACCCATCTGTCAACCTTGGACAGCGCCCAACCC	780
Db	721	ATGAGAGCTCTGACCCCAACCAACGGGCCACCCATCTGTCAACCTTGGACAGCGCCCAACCC	780
OY	781	CTTCTAGACACTCTGTGACACAGTGAAGAAATGTGACACGCTGCAGTTGGTGGGTAAACGC	840
Db	781	CTTCTAGACACTCTGTGACACAGTGAAGAAATGTGACACGCTGCAGTTGGTGGGTAAACGC	840
OY	841	TGGACCCCTGTGCTACCCCGAGACCCAGAGAGGCTCTGCCCCGAGGTGACATGTCTGTGG	900
Db	841	TGGACCCCTGTGCTACCCCGAGACCCAGAGAGGCTCTGCCCCGAGGTGACATGTCTGTGG	900
OY	901	GACCAAGTTGCCACAGACAGCTCTTTGGCCCCGCTGTCTGTGGCCCAACTCTCTGCCAAGATCC	960
Db	901	GACCAAGTTGCCACAGACAGCTCTTTGGCCCCGCTGTCTGTGGCCCAACTCTCTGCCAAGATCC	960
OY	961	CCACCCCGGCTGCGCAGCATGATGTGTGCAACCGGGGCCGACGTCTACACACTGTATGTGAC	1020
Db	961	CCACCCCGGCTGCGCAGCATGATGTGTGCAACCGGGGCCGACACTCTACACACTGTATGTGAC	1020
OY	1021	CGCGTCCCAAGCGCGGCTGTGAAGAGATTGTGTGCGACGCTGTGGGCTGTGCGAGGCAAG	1080
Db	1021	CGCGTCCCAAGCGCGGCTGTGAAGAGATTGTGTGCGACGCTGTGGGCTGTGCGAGGCAAG	1080
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Db	1081	ATGCAAGCCGTGGAGGTGGAGATGTGGCGGCTTCCGAGACACAGTACAGATGATGTCTCAG	1140
OY	1141	CGCTGGGCGCCAGCAGCAGCCCGGGGCTGTGAGAGCCGTTTACGCGGCCCCCTGGAGGCGCATG	1200
Db	1141	CGCTGGGCGCCAGCAGCAGCCCGGGGCTGTGAGAGCCGTTTACGCGGCCCCCTGGAGGCGCATG	1200
OY	1201	GGGCTGTGACAGGCTGTGTGTGAAGACTTGTGCGACGCGCCTCTCAGCGCGGCCCCGTGA	1254
Db	1201	GGGCTGTGACAGGCTGTGTGTGAAGACTTGTGCGACGCGCCTCTCAGCGCGGCCCCGTGA	1254

RESULT	4	HSU74611	1634 bp	mRNA	PRI	02-JAN-1997
LOCUS	HSU74611	1634 bp	mRNA			
DEFINITION	Human Apo-3 mRNA, complete cds.					
ACCESSION	U74611					
VERSION	U74611.1	GI:1763292				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 1634)					
TITLE	Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,					
JOURNAL	Goddard,A.D., Bauer,K.D. and Ashkenazi,A.					
REFERENCE	Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kB					
AUTHORS	Cur. Biol. (1996) In press					
JOURNAL	2 (bases 1 to 1634)					
TITLE	Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,					
REFERENCE	Goddard,A.D., Bauer,K.D. and Ashkenazi,A.					
AUTHORS	Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San					
JOURNAL	Bruno Blvd., South San Francisco, CA 94080, USA					
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Matches 1254;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Db	389	CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCGTGGCGCTGAAGCCAGGC	448
QY	361	TGCCTTGTGAGAGTGGCCAGGCTCAGCCAAATGTCAGCAGTTCAACCCCTTCTACTGCCAACCA	420
Db	449	TGGTTTGTGGAGTGCACAGGTCAGCCAAATGTCAGCAGTTCAACCCCTTCTACTGCCAACCA	508
QY	421	TTCCTAGACTGCGGGGCCCTTGACACCGCCACACACGGCTACTCTGTTCCCGCAGAGTACT	480
Db	509	TGCCTAGACTGCGGGGCCCTTGACACCGCCACACACGGCTACTCTGTTCCCGCAGAGTACT	568
QY	481	GACTGTGGAGACCTCCCTGCGCTTCTTAAGACATGGGAGATGGCGGTGCCTGTCGCGCC	540
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QY	661	ACCCACACATACCGCCGACCTGTGGGCTGCACAAACCCCTGGTTACTGTGCAGATTAACCTGG	720
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QY	901	GACCAAGTTGCCAGCAGAGCTCTTGGCCCGCGCTGCTGCGCCACACACTCTGCCAGAGATCC	960
Db	989	GACCAAGTTGCCAGCAGAGCTCTTGGCCCGCGCTGCTGCGCCACACACTCTGCCAGAGATCC	1048
QY	961	CCAGCCGGCTCCGCCAGCATGATGCTGACAGCCGGGCGCCGACCTCTACGACCTGATGGAC	1020
Db	1049	CCAGCCGGCTCCGCCAGCATGATGCTGACAGCCGGGCGCCGACCTCTACGACCTGATGGAC	1108
QY	1021	GGGCTCCCAACGGGCGGTGGGAAGGATTCGTGCGACAGCTGGGGCTGGCGAGGCACAG	1080
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QY	1081	ATCGAAGCGCTGGAGGTGGAGATCGGCCGCTTCCGAGACACAGCAGTACGAGATGCTCAAG	1140
Db	1169	ATCGAAGCGCTGGAGGTGGAGATCGGCCGCTTCCGAGACACAGCAGTACGAGATGCTCAAG	1228
QY	1141	CGCTGGCGCCAGCAGCAGACCCCGGGGCTCTCGAGACCGTTTACGGGGCCCTGGAGCGCATG	1200
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QY	1201	GGGCTGGAGCGGTGCGTGAAGACTTGGCCACGCGGCTTCCACAGCGGGCCCGGTGA	1254
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RESULT	5		
LOCUS	HSU94502	1257 bp	mRNA
DEFINITION	Human lymphocyte associated receptor of death 1b mRNA,		
ACCESSION	U94502	1	GI:2071950

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1257)
McMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
2 (bases 1 to 1257)
Screation, G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

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Best local Similarity 99.8%; Pred. No. 3.8e-202;
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RESULT 6
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LOCUS HS083597 1528 bp mRNA PRI 27-JAN-1997
DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

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Db	421	CCCTGcACcCGcCAGAcACAGcGgCTACTCTGTtTCCGcAGATACTAGTGTGGACCTGcC	480

QY	497	TGCTGGCTTTATGAAACATGGGAGATGGGCGCGTCTGCCCCAGAGACACCTGGGGGA	556
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QY	857	CCGAGACCCAGAGGGGGCTGTGCCCGAGGATGACATGGTCTGGGACACAGTTGGCCAGCA	916
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QY	917	GAGCTTTTGGCCCGCTGCTGCTGCGCCACACACTCTCGCCAGAGTCCCCAGCGGCTGCGCAG	976
Db	901	GAGCTTTTGGCCCGCTGCTGCTGCGCCACACACTCTCGCCAGAGTCCCCAGCGGCTGCGCAG	960
QY	977	CCATGATGCTGCAGAGCCGGGCGCCGACGCTTACAGACGTGATGAGACGGGCTCCAGCGGGC	1036
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QY	1037	GCTGGAAGAGATTGCTGTCGCGACGCTGGGGCTGGCGCGAGGAGAGATGGAACCCGTGGAGG	1096
Db	1021	GCTGGAAGAGATTGCTGTCGCGACGCTGGGGCTGGCGCGAGGAGAGATGGAACCCGTGGAGG	1080
QY	1097	TGGAGATCGGCGCCTTCCGAGACAGCAGTACAGATGCTCAAGCGCTGGCGCCAGCAGC	1156
Db	1081	TGGAGATCGGCGCCTTCCGAGACAGCAGTACAGATGCTCAAGCGCTGGCGCCAGCAGC	1140
QY	1157	AGCCCGCGGGCCTTCGGAGCCGTTTACGCGGGCCCTGGAGCGCATGSGGCTGGAGCGGCTGCG	1216
Db	1141	AACCCCGGGGCTTCGGAGCGCTTACGCGGGCCCTGGAGCGCATGSGGCTGGAGCGGCTGCG	1200
QY	1217	TGGAAGACTTGGCGAGCGCGCTGAGCGGGCGCCGTGA 1254	
Db	1201	TGGAAGACTTGGCGAGCGCGCTGAGCGGGCGCCGTGA 1238	
RESULT	7		
LOCUS	HSU75380	1557 bp mRNA	PRI 05-Apr-1997
DEFINITION	Human apoptosis-mediating receptor TRAMP mRNA, partial cds.		
ACCESSION	U75380		
VERSION	U75380.1	GI:1695924	
KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1557) Bodmer, J. L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Borman, T., Hahne, M., Schroter, M., Becker, K., Wilson, A., Frensch, L. E., Browning, J. L., MacDonald, R. and Tschopp, J.		
TITLE	TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)		
JOURNAL	Immunoty 6 (1), 79-88 (1997)		
MEDLINE	97205335		

AUTHORS

Screaton, G.R.
 TITLE Direct Submission
 Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
 JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
 9DU, UK

FEATURES

Source Location/Qualifiers

CDS

1..1355
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 /db_xref="taxon:9606"
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 /note="LARD-2, similar to Fas and TNF-R1, probably
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 /note="Insertion compared to LARD 1a, deposited in Genbank
 Accession Number U94501, probable retained intron leading
 to premature transcriptional termination"

BASE COUNT 223 a 441 c 451 g 240 t
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Query Match 91.1%; Score 1143; DB 11; Length 1355;
 Best Local Similarity 92.5%; Pred. No. 1.8e-185;

Matches 1254; Conservative 0; Mismatches 0; Indels 101; Gaps 1;

QY 1 ATGGAGCAGCGCGCGGGGCTGCGGGGGTGGCGGCGCGCTCTCTGCTGCTG 60
 Db 1 ATGGAGCAGCGCGCGGGGCTGCGGGGGTGGCGGCGCGCTCTCTGCTGCTG 60
 QY 61 GGGGCGCGCGCGCGAGGGGGGCTGTAGCCCGAGGTGTGACTGTGCGGTACTTCCAC 120
 Db 61 GGGGCGCGCGCGCGAGGGGGGCTGTAGCCCGAGGTGTGACTGTGCGGTACTTCCAC 120
 QY 121 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACACTGTAAGGCCCT 180
 Db 121 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACACTGTAAGGCCCT 180
 QY 181 TGACAGGAGCCCTGGCGCACTCACTGCTTGTGTGCCCAAGACACTTCTTGAGCC 240
 Db 181 TGACAGGAGCCCTGGCGCACTCACTGCTTGTGTGCCCAAGACACTTCTTGAGCC 240
 QY 241 TGGGAGAACCACTAATTGTGATGTGCCGCTGCCAGGCTGTGATGAGAGGCTTC 300
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 QY 301 CAGGAGGCGTGGAGAACTGTTACAGAGGCGGACACCGCGCTGGTGAAGCCAGGC 360
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 QY 541 ACGAGCACTTGGGAGCTGTCCAGAGGCGTGTGCGCTGTCTGTGGCTGAGGAGAGA-- 598

Db 541 ACGAGCACTTGGGAGCTGTCCAGAGCGGTGTGCGCTGTGCTGAGGAGAGAGT 600
 QY 599 -----
 Db 601 AGGTGTGTCTGGGAATGCGAGTGGAGAACTGGGATGGACCGGAGGAGCGGTGAG 660
 QY 599 -----TGTTCTGGGTCCAGTGTCTC 619
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 QY 620 TGGCTGGCTTGTGTGTCCT 679
 Db 721 TGGCTGGCTTGTGTGTCCT 780
 QY 680 GCTGGGCTCAAGAGCCCTGCTGTACAGAGTGAATGAACCTGGAGTGGAGGCTCTACCCAC 739
 Db 781 GCTGGGCTCAAGAGCCCTGCTGTACAGAGTGAATGAACCTGGAGTGGAGGCTCTACCCAC 840
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 Db 961 AGACCCAGAGAGGCTCTGCGCGCAGTGTGATGATGATGATGATGATGATGATGATGAT 1020
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 Db 1021 CTCTTGGCCCGCTGTGCGCCACACTCTGCGCAGAGTCCGACGCGGCTGCGCACCA 1080
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 Db 1081 TGAATGTGAGCCGCGCGCAGACTTACAGACTGTATGAGAGCGGCTGCCAGCGCGCT 1140
 QY 1040 GGAAGAGATTCTGTCGCGCAGCTGGGCTGCGCGAGCAGAGATGGAAGCCGTGAGGTG 1099
 Db 1141 GGAAGAGATTCTGTCGCGCAGCTGGGCTGCGCGAGCAGAGATGGAAGCCGTGAGGTG 1200
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 QY 1160 CCGGGGCTTGGAGCGCTTTACGCGGCTTGGAGCGCATGGGCTGAGCGCTGCTG 1219
 Db 1261 CCGGGGCTTGGAGCGCTTTACGCGGCTTGGAGCGCATGGGCTGAGCGCTGCTG 1320
 QY 1220 AAGACTTGGGAGCCGCTGCAAGCGGCGCGTGA 1254
 Db 1321 AAGACTTGGGAGCCGCTGCAAGCGGCGCGTGA 1355

RESULT 10

HSMSL1
 LOCUS HSMSL1 1743 bp mRNA PRI 16-DEC-1996
 DEFINITION H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.
 ACCESSION Y09392.1
 VERSION Y09392.1 GI:1669690
 KEYWORDS WSL-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 (bases 1 to 1743)
 Kitson, J., Raven, T., Jiang, Y.P., Goeddel, D.V., Giles, K.M.,
 Pun, K.T., Grimham, C.J., Brown, R. and Farrow, S.N.
 A death-domain-containing receptor that mediates apoptosis
 JOURNAL Nature 384 (6607), 372-375 (1996)
 MEDLINE 97088617

Db 1149 TGATGCTGACCCGCGCCGAGCTCTACGACGTGATGAGCGGCTCCAGCGCGCCT 1208
QY 1040 GGAAGAGATTGCTGCGACGCTGGGGCTGCGCGAGCGAGATGAGCCGCGAGGCTGG 1099
Db 1209 GGAAGAGATTGCTGCGACGCTGGGGCTGCGCGAGCGAGATGAGCCGCGAGGCTGG 1268
QY 1100 AGATGCGCGCTTCCGAGACGAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGC 1159
Db 1269 AGATGCGCTTCCGAGACGAGTACGAGATGCTCAAGCAGCTGGCGCCAGCAGCAGC 1328
QY 1160 CCGCGGGCTTCCGAGACGCTTACGCGCGCTTGGAGCGCATGGGCTGAGCGCTCGTGG 1219
Db 1329 CCGCGGGCTTCCGAGACGCTTACGCGCGCTTGGAGCGCATGGGCTGAGCGCTCGTGG 1388
QY 1220 AAGACTGCGCGCGCTGCGAGCGCGCGCTGA 1254
Db 1389 AAGACTGCGCGCGCTGCGAGCGCTGAGCGCTGA 1423

RESULT 11
LOCUS HSU94504 1198 bp mRNA PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 3 mRNA, alternatively spliced, complete cds.
ACCESSION U94504
VERSION U94504.1 GI:2071954
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Sreteron, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., McMichael, A.J. and Bell, J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
REFERENCE 2 (bases 1 to 1198)
AUTHORS Sreteron, G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

FEATURES
source location/Qualifiers
1. 1198
/organism="Homo sapiens"
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/cell_line="HeLa"
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Query Match 90.3%; Score 1132; DB 11; Length 1198;
Best Local Similarity 95.5%; Pred. No. 1.4e-183;

Matches 1198; Conservative 0; Mismatches 0; Indels 56; Gaps 1;
QY 1 ATGAGACACAGGCGCGGGGCTGCGCGGCTGAGCGGCGGCGGCTCTCTGAGTGTGCTG 60
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QY 361 TGGTTGTGAGAGTGCAGGTCAGCCCAATGTGTGAGCAGTTACACCTTCTACTCCAAACA 420
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QY 545 TTCTGGGTCCAGTGTCTCTGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604
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Db 665 ATGAGAGCTGTGACCCACACCGCCACCGCATCTGTGACCGCTTGGACAGCGCCACAC 724
QY 781 CTTCTAGACACTCTGACAGCACTGAGAAAGATGTGACCGCTGAGTTGTGGTAAACAGC 840
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LOCUS	Homo sapiens	soluble death receptor 3 beta (DR3)	complete cds.
DEFINITION	AF026071		
ACCESSION	AF026071.1	GI:2570832	
VERSION			
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Primates; Hominidae; Homo. (bases 1 to 1763)		
AUTHORS	Matzocza,K., Ribeiro,P., Renard,N., Chalot,C., Colflier,B. and Salles,G.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-Sep-1997) Hematology, CTR Hospitalier Lyon-Sud, Chemin du Grand Revoyet, Pierre Benite 69495, France		
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CDS			
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BASE COUNT			
ORIGIN			
Query Match	88.0%;	Score 1103.4;	DB 11; Length 1763;
Best Local Similarity	90.8%;	Pred. No. 9e-179;	
Matches 1248;	Conservative 0;	Mismatches 6;	Indels 121; Gaps 2;
QY	1	ATGAGACAGCGCGCGGCGCTGCGCGCGCGCGCGCGCGCGCTCTCTCTGCTGCTG	60
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QY	61	GGGCGCGCGCGCGCGCGCGCGCTGTAAGCCCAAGTGTGACTGCGCGGTACTTCAC	120
Db	129	GGGCGCGCGCGCGCGCGCGCGCTGTAAGCCCAAGTGTGACTGCGCGGTACTTCAC	188

OY	121	AAGAAGATTGGCTGTTTGTGTCAGAGGCTGCACAGCGGGAGCACTACTGAAGCCCT	180
Db	189	AAGAAGATTGGCTGTTTGTGTCAGAGGCTGCCAACCGGGAGCACTACTGAAGCCCT	248
OY	181	TGCACGAGCCTCTCGGCACATCTCACCTGCTGTGTGTCTCCCAAGACACTTCTTGACC	240
Db	249	TGCACGAGCCTCTCGGCACATCTCACCTGCTGTGTGTCTCCCAAGACACTTCTTGACC	308
OY	241	TGGGAAGAACCACTTAATTCTGAATGTGCCCCGTGCCAGGCTGTGTATACAGAGCTTC	300
Db	309	TGGGAAGAACCACTTAATTCTGAATGTGCCCCGTGCCAGGCTGTGTATAGGAGAGGCTTC	368
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Db	369	CAGGAGGCGCTGGGAAGACTGTTCAGCATGTGGCCAGACACCGCGTGGGCTGAAGCCAGGC	428
OY	361	TGTGTTGTGAGATCCAGAGTCAGCAATGTGTACAGAGTTCACCTCTACTAGCCAACA	420
Db	429	TGTGTTGTGAGATCCAGAGTCAGCAATGTGTACAGAGTTCACCTCTACTAGCCAACA	488
OY	421	TGCCTAGACTCGGGGGCCCTGACACCGGCACACAGGCTACTGTTCGCCGAGAGATACT	480
Db	489	TGCCTAGACTCGGGGGCCCTGACACCGGCACACAGGCTACTGTTCGCCGAGAGATACT	548
OY	481	GACTGTGGGAACTGCTGCTGCTGTATGAACAATGGGAGTGGCTGTCTGCTGCC	540
Db	549	GACTGTGGGAACTGCTGCTGCTGTATGAACAATGGGAGTGGCTGTCTGCTGCC	608
OY	541	AC-----GAGCACCCCTGGGGAGCTGTCCAGAGGCTGTGGCCGTG	580
Db	609	ACGCCACCCCGTCTCCCTTGCAGAGAGCACCTGGGGAGCTGTCCAGAGGCTGTGGCCGTG	668
OY	581	TCTGTGCTGGAGGACAGA-----	598
Db	669	TCTGTGCTGGAGGACAGATAGTGTGTCTGGGAATGCGGTGGAGAACTGGGATATGG	728
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Db	729	ACCGAAGGAGGCGGGTAGAGAGGGGGGCACCAACCCACACACACACTCTTTCAGT	788
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Db	789	GTTCTGGGTCAGAGTGCCTCGGTGGCTCTGTGTGTCTCCCTCTCTGAGGGCCACACT	848
OY	660	GACCTACACATACCGGCACACTGCTGTGCCTCAAGCCCTGTGTTACTGAGATGAAGCTGG	719
Db	849	GACCTACACATACCGGCACACTGCTGTGCCTCAAGCCCTGTGTTACTGAGATGAAGCTGG	908
OY	720	GATGAGAGGCTGTGACCCCACACCAGGCCACCATCTGTACACCTTGGAGACGGCCACAC	779
Db	909	GATGAGAGGCTGTGACCCCACACCAGGCCACCATCTGTACACCTTGGAGACGGCCACAC	968
OY	780	CCTTCTAGCACTCTCTACAGAGAGTAGAAGATCTGACACCTCCAGTTGGTGGGTAAACAG	839
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Db 1269 GATCGAAGCCGTGAGGTGAGATCGCTCTCTCTCCGAGACAGACAGATGAGATGCTCAA 1328
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Db 1329 GCACTGGCGCAGACAGAGCCCGGGGGCTTCGAGAGCCGTTACAGCGCGCCGTCGAGCGCAT 1388
QY 1200 GGGGCTGGAGCGCTGCTGGAAGACTTGCAGAGCCGCTCGACGCGCGCCGCTGA 1254
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RESULT 13
HSU94510 1143 bp mRNA PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 9 mRNA, alternatively
DEFINITION
ACCESSION 094510
VERSION 094510.1 GI:2071966
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1143)
TITLE Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 9727273
MEDLINE 2 (bases 1 to 1143)
REFERENCE Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
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/db_xref="taxon:9606"
/cell_line="Hela"
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1. 1143
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598..599
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"
misc_feature
BASE COUNT 188 a 378 c 378 g 199 t
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Best Local Similarity 91.1%; Pred. No. 7.2e-165;
Matches 1143; Conservative 0; Mismatches 0; Indels 11; Gaps 1;
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Db 1 ATGAGACAGCGCGCGCGGCTGGCGGCGGTGGCGCGCGGCTCTCTGCTGCTG 60

QY 61 GGGGCCCCGGCCAGAGCGGCGCACTGTACCCAGGTGTGACTGTCCGGTACTTCCAC 120
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Db 121 AAGAAATTTGCTGCTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCT 180
QY 181 TGCACGAGGACCTTGGGGCAACTCCACCTGTGTGTGCCCAAGACACTTCTTGGCC 240
Db 181 TGCACGAGGACCTTGGGGCAACTCCACCTGTGTGTGCCCAAGACACTTCTTGGCC 240
QY 241 TGGGAGAACACCATTAATTCGAATGTGCCCCCTGCGACGCTGTATAGCAGGCTCC 300
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Db 361 TGGTTTGGAGTGGCAGAGTGCAGCAATGTGTCAAGATTCACCCCTTATGCGCAACCA 420
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Db 421 TGCCTAGACTGGGGGCCCTGACCGCCACACAGCGGCTACTGTGTTCCCGCAGAGTACT 480
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Db 599 ----- 598
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Db 730 TGGACCCCTGCTACCCCGAGACCCAGAGGCGCTGTGCCCCGAGGTGACATGCTCTGG 789
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Db 790 GACCAATGCGCAGAGACCTCTGCGCCCGCTGCTGCGCCCAACTCTGCGCAGAGTCC 849
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RESULT 15

LOCUS HSU94505 1087 bp mRNA PRI 15-MAY-1997

DEFINITION Human lymphocyte associated receptor of death 4 mRNA, alternatively spliced, complete cds.

ACCESSION U94505

VERSION U94505.1 GI:2071956

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1087) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Screenshot,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.

TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

MEDLINE 97272273

REFERENCE 2 (bases 1 to 1087) Screenshot,G.R.

AUTHORS Direct Submission

TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of

FEATURES	Location/Qualifiers
source	1. .1087

CDS	/cell_type="lymphocyte"
	1.546

misc_feature

BASE COUNT	180 a	363 c	355 g	189 t
ORIGIN				

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Best Local Similarity	86.7%;	Pred. No. 8.2e-146;		
Matches 1087;	Conservative	0;	Mismatches	0;
			Indels	167;
			Gaps	1;

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QY	181	TGCACGAGCCCTGCGGCAACTCACCTGCTTGTGTGCCAAGACACCTTCTGGCC	240
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QY	301	CAGGTGGCGCTGGAGAACTGTTTCAGCAGTGGCGGACACCCGGCTGTGGCTGTGAAGCAGAGC	360
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QY	421	TGCTTAACCTGCGGGGGCCCTTGCACCGCCACACACGCGTACTCTGTCTTCCCGCAGAGATCT	480
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QY	541	ACGAGCACCCCTGGGGAGCTGTCCAGAGCCGTGTGCCGTGTCTGTGGCTGGAGCAGATG	600
Db	541	AC-----	542
QY	601	TTCGGGTCCAGGTGCTCCTGGGTGGCCCTTGTGTGTGCCCTCTGTGGGGCCACCGTG	660
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Db	543	-----ATGAACCTGGG	553
QY	721	ATGAGAGCTTGACCCACCACCGGCGACCCATCTGTACCTTGTGAACAGGGCCACACCC	780
Db	554	ATGAGAGCTTGACCCACCACCGGCGACCCATCTGTACCTTGTGAACAGGGCCACACCC	613
QY	781	CTTTACACCTCTCTACAGCAGTGTGAAGATCTGCACCGTCCAACTTGGTGGTAAACGC	840
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QY	841	TGCAACCTTGCTTACCCCGAGACCCAGAGAGGGCTCTGCCCGCAGGTGCATGTCTCGG	900
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QY	961	CCAGCCGGCTGCGCAGCAGCATGATGTCTGACAGCCGGGCGCCGACACTTACGACGTGATGAC	1020
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QY	1081	ATCGAAGCCGTGAGGTGTGATGTGCGCCCTTCCGAGACACAGTACAGATGCTCAAG	1140
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QY	1141	CGCTGGCGCAGACGAGCCCGCGGGGCTGTGAGAGCCGTTTACGCGGCCCTGGAGCGCATG	1200
Db	974	CGCTGGCGCAGACGAGCCCGCGGGGCTGTGAGAGCCGTTTACGCGGCCCTGGAGCGCATG	1033
QY	1201	GGGCTGGACGGCTGCGTGGAAAGCTTGGCAGCCGCTGACAGCGCGGCGCCCGGA	1254
Db	1034	GGGCTGGACGGCTGCGTGGAAAGCTTGGCAGCCGCTGACAGCGCGGCGCCCGGA	1087

Search completed: July 23, 2000, 06:51:24
Job time: 2083 sec

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Dp 61 GGGCCCGGGCCAGGGCGGCGACTCGTAGCCCCCAGGTGTGACTGTGCGCGGTGACTTCCAC 120

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DB 1201 GGGGTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
    |||
RESULT 2
ID X00925 standard; cDNA; 1254 BP.
AC X00925:
DE 25-MAR-1999 (first entry)
DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
OS Homo sapiens.
FH Key CDS
FT 1..1254
FT /tag= a
FT /product= "Death domain containing receptor DR3"
FT sig_peptide
FT 1..72
FT /tag= b
FT mat_peptide
FT 73..1251
FT /tag= c
PM J1100170-A.
PD 06-JAN-1999.
PR 12-MAR-1997; 057503.
PR 06-FEB-1997; US-037341.
PR 12-MAR-1996; US-013285.
PR 17-OCT-1996; US-028711.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNITED MICHIGAN.
DR WP1: 99-124390/11.
DR P-PSDB; W95538.
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 6; Fig 3; 50pp; Japanese.
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97457. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T;

Query Match 100.0%; Score 1254; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 4,3e-263;
Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 61 GGGGCGCGGCGCGAGGCGGCACTGTAGCCAGGTGTGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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DB 61 GGGGCGCGGCGCGAGGCGGCACTGTAGCCAGGTGTGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
OY 121 AAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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DB 121 AAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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DB 241 TGGGAGAACCAACATTAATTTGAAATGTGCCGCTGCCAGGCTGTGATGAGAGCCCTCC 300
OY 301 CAGGTGGCGCTGGAGAACTGTTCAGCAAGTGGCCAGACCCGCTGGCTGTAAAGCAGAGC 360
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DB 301 CAGGTGGCGCTGGAGAACTGTTCAGCAAGTGGCCAGACCCGCTGGCTGTAAAGCAGAGC 360
OY 361 TGGTTTGTGAGTGGCCAGAGTGCATGTCAGACATGTCAGACATGTCAGACATGTCAGACATGTCAGAC 420

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QY	541	ACGAGCACCCTGGGGAGCTGTCACAGAGCCTGTGCCGTCTGTGGCTGGAGCAATG	600
Db	629 <td>ACGAGCACCCTGGGGAGCTGTCCAGAGCCTGTGCCGTCTGTGGCTGGAGCAATG<td>688</td></td>	ACGAGCACCCTGGGGAGCTGTCCAGAGCCTGTGCCGTCTGTGGCTGGAGCAATG <td>688</td>	688
QY	601 <td>TTCTGGGTCAGAGTGCTCTCTGGCTGGCTTTGGTCCCTCTCTGTTGGGCCACCTTG<td>660</td></td>	TTCTGGGTCAGAGTGCTCTCTGGCTGGCTTTGGTCCCTCTCTGTTGGGCCACCTTG <td>660</td>	660
Db	689 <td>TTCTGGGTCAGAGTGCTCTCTGGCTGGCTTTGGTCCCTCTCTGTTGGGGCCACCTTG<td>748</td></td>	TTCTGGGTCAGAGTGCTCTCTGGCTGGCTTTGGTCCCTCTCTGTTGGGGCCACCTTG <td>748</td>	748
QY	661 <td>ACCTACACATACCCGCCACACGTCTGGCCCTCACAAACCCCTGGTTACTGAGATGAAAGCTGGG<td>720</td></td>	ACCTACACATACCCGCCACACGTCTGGCCCTCACAAACCCCTGGTTACTGAGATGAAAGCTGGG <td>720</td>	720
Db	749 <td>ACCTACACATACCCGCCACACGTCTGGCCCTCACAAACCCCTGGTTACTGAGATGAAAGCTGGG<td>808</td></td>	ACCTACACATACCCGCCACACGTCTGGCCCTCACAAACCCCTGGTTACTGAGATGAAAGCTGGG <td>808</td>	808
QY	721 <td>ATGAGAGCTCTGTGACCCACACACCGGACACCACCTATCTGTCACTCTTGGAGACAGCCACACC<td>780</td></td>	ATGAGAGCTCTGTGACCCACACACCGGACACCACCTATCTGTCACTCTTGGAGACAGCCACACC <td>780</td>	780
Db	809 <td>ATGAGAGCTCTGTGACCCACACACCGGACACCACCTATCTGTCACTCTTGGAGACAGCCACACC<td>868</td></td>	ATGAGAGCTCTGTGACCCACACACCGGACACCACCTATCTGTCACTCTTGGAGACAGCCACACC <td>868</td>	868
QY	781 <td>CTTTAGACACCTCTCTGACAGACAGTGAAGAGATCTGCACCGTCCAGTTGGTGGTAAACAGC<td>840</td></td>	CTTTAGACACCTCTCTGACAGACAGTGAAGAGATCTGCACCGTCCAGTTGGTGGTAAACAGC <td>840</td>	840
Db	869 <td>CTTTAGACACCTCTCTGACAGACAGTGAAGAGATCTGCACCGTCCAGTTGGTGGTAAACAGC<td>928</td></td>	CTTTAGACACCTCTCTGACAGACAGTGAAGAGATCTGCACCGTCCAGTTGGTGGTAAACAGC <td>928</td>	928
QY	841 <td>TGGACCCCTTGGCTTACCCCGACAGCCACAGAGAGCCCTGTGCCCGGACAGTGAATGGTCCMG<td>900</td></td>	TGGACCCCTTGGCTTACCCCGACAGCCACAGAGAGCCCTGTGCCCGGACAGTGAATGGTCCMG <td>900</td>	900
Db	929 <td>TGGACCCCTTGGCTTACCCCGACAGCCACAGAGAGCCCTGTGCCCGGACAGTGAATGGTCCMG<td>988</td></td>	TGGACCCCTTGGCTTACCCCGACAGCCACAGAGAGCCCTGTGCCCGGACAGTGAATGGTCCMG <td>988</td>	988
QY	901 <td>GACCACTTCCCGACAGAGCTCTTGGCCCGCGCTGTGCGGCCACACACTCTGCCAGAGTCC<td>960</td></td>	GACCACTTCCCGACAGAGCTCTTGGCCCGCGCTGTGCGGCCACACACTCTGCCAGAGTCC <td>960</td>	960
Db	989 <td>GACCACTTCCCGACAGAGCTCTTGGCCCGCGCTGTGCGGCCACACACTCTGCCAGAGTCC<td>1048</td></td>	GACCACTTCCCGACAGAGCTCTTGGCCCGCGCTGTGCGGCCACACACTCTGCCAGAGTCC <td>1048</td>	1048
QY	961 <td>CCAGCCGGCTCGCCACAGCCATGATGTCTGACACCGGAGCCCGGACAGCTCTACAGAGTATGAGC<td>1020</td></td>	CCAGCCGGCTCGCCACAGCCATGATGTCTGACACCGGAGCCCGGACAGCTCTACAGAGTATGAGC <td>1020</td>	1020
Db	1049 <td>CCAGCCGGCTCGCCACAGCCATGATGTCTGACACCGGAGCCCGGACAGCTCTACAGAGTATGAGC<td>1108</td></td>	CCAGCCGGCTCGCCACAGCCATGATGTCTGACACCGGAGCCCGGACAGCTCTACAGAGTATGAGC <td>1108</td>	1108
QY	1021 <td>GCGGTCACAGCGCGGCGCTGGAAGAGATTGTGTGGACAGCTGGGAGCTGGCGAGGACAGAG<td>1080</td></td>	GCGGTCACAGCGCGGCGCTGGAAGAGATTGTGTGGACAGCTGGGAGCTGGCGAGGACAGAG <td>1080</td>	1080
Db	1109 <td>GCGGTCACAGCGCGGCGCTGGAAGAGATTGTGTGGACAGCTGGGAGCTGGCGAGGACAGAG<td>1168</td></td>	GCGGTCACAGCGCGGCGCTGGAAGAGATTGTGTGGACAGCTGGGAGCTGGCGAGGACAGAG <td>1168</td>	1168
QY	1081 <td>ATCGAAGCCGTGAGAGTGTGAGATCGGCCGCTTCCGAGACCAAGCAGTACGAGATGCTCAAG<td>1140</td></td>	ATCGAAGCCGTGAGAGTGTGAGATCGGCCGCTTCCGAGACCAAGCAGTACGAGATGCTCAAG <td>1140</td>	1140
Db	1169 <td>ATCGAAGCCGTGAGAGTGTGAGATCGGCCGCTTCCGAGACCAAGCAGTACGAGATGCTCAAG<td>1228</td></td>	ATCGAAGCCGTGAGAGTGTGAGATCGGCCGCTTCCGAGACCAAGCAGTACGAGATGCTCAAG <td>1228</td>	1228
QY	1141 <td>CCTGCGCCGACAGACAGACAGCCCGGCGGCTCTGGAGACCTTTTACGGGGCCCTGGAGAGCATG<td>1200</td></td>	CCTGCGCCGACAGACAGACAGCCCGGCGGCTCTGGAGACCTTTTACGGGGCCCTGGAGAGCATG <td>1200</td>	1200
Db	1229 <td>CCTGCGCCGACAGACAGACAGCCCGGCGGCTCTGGAGACCTTTTACGGGGCCCTGGAGAGCATG<td>1288</td></td>	CCTGCGCCGACAGACAGACAGCCCGGCGGCTCTGGAGACCTTTTACGGGGCCCTGGAGAGCATG <td>1288</td>	1288
QY	1201 <td>GGGCTGAGAGCGCTGCGGTGAAGACTTCCGACAGCGCGCTGACAGCGCGGCCCTGTGA<td>1254</td></td>	GGGCTGAGAGCGCTGCGGTGAAGACTTCCGACAGCGCGCTGACAGCGCGGCCCTGTGA <td>1254</td>	1254
Db	1289 <td>GGGCTGAGAGCGCTGCGGTGAAGACTTCCGACAGCGCGCGCTGACAGCGCGGCCCTGTGA<td>1342</td></td>	GGGCTGAGAGCGCTGCGGTGAAGACTTCCGACAGCGCGCGCTGACAGCGCGGCCCTGTGA <td>1342</td>	1342

RESULT 4

V28700 ID V28700 standard; cDNA; 1847 BP.

AC V28700; DT 20-AUG-1998 (first entry)

DE Human apoptosis inducing receptor coding sequence.

KW Apoptosis inducing receptor; AIR protein; human; cell death regulator; Type I transmembrane protein; tumour cell death; autoimmune disease;

KM therapy: ss.

OS Homo sapiens.

PH key

FT CDS Location/Qualifiers

FT /tag= a

FT /product= AIR

MO9814565-A1.

PD 09-APR-1998.

PF 03-OCT-1997; U17876.

PR 04-OCT-1996; ~~BB-044456~~

PA (IMM IMMEX-CORP.

PI Perkins PA;

DR WPI: 98-240077/21.

DR P-PSDB: W57045.

PT DNA encoding apoptosis inducing receptor - which is Type I

transmembrane protein, useful for regulating cell death
 PT Claim 2: Page 28-30: 45PP: English.
 CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
 CC invention. AIR is a type I transmembrane protein, soluble forms of which
 CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
 CC can also be used *in vitro* to block apoptosis or AIR-expressing cells, or
 CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
 CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
 CC death, which is useful to regulate cell death in a therapeutic setting
 CC well as *in vitro*. Agonists of AIR activity can be used to kill tumour
 CC cells that express AIR, or T cells expressing AIR in autoimmune diseases
 SQ Sequence 1847 Bp, 316 A, 605 C, 579 G, 347 T;

Query Match	100.0%;	Score 1254;	DB 1;	length 1847;
Best Local Similarity	100.0%;	Pred. No. 4.6e-263;		
Matches 1254;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGAGCACACGGGCGGGGGCTGCGGGGGGTGGGGGGGGCGCTCCCTCGTGTGCTG	60
Db	236	ATGGAGCACACGGGCGGGGGCTGCGGGGGGTGGGGGGGGCGCTCCCTCGTGTGCTG	295
QY	61	GGGGCGGGGGCCCGAGGGCGGCACTCGTAGGCCCGAGGTGTGACTGTGGCGGTTCCAC	120
Db	296	GGGGCGGGGGCCCGAGGGCGGCACTCGTAGGCCCGAGGTGTGACTGTGGCGGTTCCAC	355
QY	121	AAGAAATATGTGCTGTTTGTGTTCACAGGGTGGCCAGCGGGGGGACATACCGGAAGGCCCT	180
Db	356	AAGAAATATGTGCTGTTTGTGTTCACAGGGTGGCCAGCGGGGGGACATACCGGAAGGCCCT	415
QY	181	TGCACGGAGCCCTGCGGGCAACTCACCTGCTGTGTGTCCCAAGACACCTTCTTGCC	240
Db	416	TGCACGGAGCCCTGCGGGCAACTCACCTGCTGTGTGTCCCAAGACACCTTCTTGCC	475
QY	241	TGGGAGAACCCATTAATTCGTGAATGTGCCGCTGCCAGGCCCTGTGATGAGCAGGGCTCC	300
Db	476	TGGGAGAACCCATTAATTCGTGAATGTGCCGCTGCCAGGCCCTGTGATGAGCAGGGCTCC	535
QY	301	CAGGTGGCGGTGAGAACTTTTCAGCAGTGGCGGACACCGCGTGGCTGTAAAGCCAGGC	360
Db	536	CAGGTGGCGGTGAGAACTTTTCAGCAGTGGCGGACACCGCGTGGCTGTAAAGCCAGGC	595
QY	361	TGGTTTGTGAGTGGCAGGTCAAGCCAAATGTGCAGCAGTTTACCCCTTCTACTGCCAACCA	420
Db	596	TGGTTTGTGAGTGGCAGGTCAAGCCAAATGTGCAGCAGTTTACCCCTTCTACTGCCAACCA	655
QY	421	TGGCTTAGACTGGGGGCCCTTCGACCGCCACACACGGGTACTGTTCCCGAGAGTACT	480
Db	656	TGGCTTAGACTGGGGGCCCTTCGACCGCCACACACGGGTACTGTTCCCGAGAGTACT	715
QY	481	GACTGTGGGACCTGCGCTGCTCGCTTCTATGAACATGGCGATGGCTCGTGTCCCTGCC	540
Db	716	GACTGTGGGACCTGCGCTGCTCGCTTCTATGAACATGGCGATGGCTCGTGTCCCTGCC	775
QY	541	ACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGGAGGCAATG	600
Db	776	ACGAGCACCCCTGGGGAGCTGTCCAGAGCGGTGTGCCGTGTCTGTGGCTGGAGGCAATG	835
QY	601	TTCTGGGTCCAGGNGCTCTGTGCTGGGCTGTGTGTCCCTCCCTGCTTGGGGGCAACCTG	660
Db	836	TTCTGGGTCCAGGNGCTCTGTGCTGGGCTGTGTGTCCCTCCCTGCTTGGGGGCAACCTG	895
QY	661	ACCTACACATACCGCACACTGCTGGCTTCACAAAGCCCTGTGTTACTGCAGATGAAGTGGG	720
Db	896	ACCTACACATACCGCACACTGCTGGCTTCACAAAGCCCTGTGTTACTGCAGATGAAGTGGG	955
QY	721	ATGAGAGCTTGAACCCACACACGGGCCACCCATGTGTACCCCTTGGGACAGGGCCACACC	780
Db	956	ATGAGAGCTTGAACCCACACACGGGCCACCCATGTGTACCCCTTGGGACAGGGCCACACC	1015
QY	781	CTTCTACACCTCTGTGACAGAGTGAAGAATGTGCACCGTCAAGTTGGTGGGTAAACGC	840
Db	1016	CTTCTACACCTCTGTGACAGAGTGAAGAATGTGCACCGTCAAGTTGGTGGGTAAACGC	1075

Db 1215 CTGACGCGGCGCCGAGCTCTAAGACGTATGAGACGCGGTCCAGCGCGCGCTGGAAAG 1274
QY 1045 GAGTTGCTGGCAGCGCTGGGGGCTGCCGAGACAGATGCCAAGCCGCTGGAGTGGAGATC 1104
Db 1275 GAGTTGCTGGCAGCGCTGGGGGCTGCCGAGACAGATGCCAAGCCGCTGGAGTGGAGATC 1334
QY 1105 GGGCGCTTCGAGACACGAGTACGATGCTCAAGCGCTGGGCCACAGACACCGCGC 1164
Db 1335 GGGCGCTTCGAGACACGAGTACGATGCTCAAGCGCTGGGCCACAGACACCGCGC 1394
QY 1165 GGGCTTCGAGACCGCTTTACGCGCGCTGGAGCGCATGGGGCTGAGACGCTGCTGTAAGAC 1224
Db 1395 GGGCTTCGAGACCGCTTTACGCGCGCTGGAGCGCATGGGGCTGAGACGCTGCTGTAAGAC 1454
QY 1225 TTGGCGACGCGCGCTGACGCGCGCGCTGGA 1254
Db 1455 TTGGCGACGCGCGCTGACGCGCGCGCTGGA 1484

RESULT 6

Id X00924 standard; cDNA; 1783 BP.
AC X00924;
DT 25-MAR-1999 (first entry)
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
KW Homo sapiens. receptor; DR3-V1; DR3; recombinant; ds.
OS Homo sapiens. Location/Qualifiers
FT Key 198..1484
FT CDS
FT sig_peptide /product= "Death domain containing receptor DR3-V1"
FT 198..300
FT 301..1481
FT mat_peptide /tag- c
FT j11000170-A.
PN 06-JAN-1999.
PD 06-MAR-1997; 057503.
PF 12-MAR-1997; US-037341.
PR 06-FEB-1997; US-013285.
PR 12-MAR-1996; US-013285.
PR 17-OCT-1996; US-028711.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ONMI) UNIV MICHIGAN.
DR WPI; 99-124390/11.
DR P-PSDB; W95537.
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 2; Fig 1, 2; 50bp; Japanese.
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-V1).
Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T;

Query Match 97.1%; Score 1217.2; DB 1; Length 1783;
Best Local Similarity 99.3%; Pred. No. 4.2e-253;
Matches 1222; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 25 GCGGGGCTGGGGGCGCTCTCTCGTGGTGTGGGGGCCGAGGCGGCACT 84
Db 255 GACCTGTGCCCCCAGGCGCTCTCTCTGTGCTGTGGGGGCCGAGGCGGCACT 314
QY 85 CGTAGCCCCAGGTGTGACTGTGCGCGGTGACTTCACACAGAGATTGCTGTTTTGTTGC 144
Db 315 CGTAGCCCCAGGTGTGACTGTGCGCGGTGACTTCACACAGAGATTGCTGTTTTGTTGC 374
QY 145 AGAGGCTGCCAGCGGGGCACTACTGAAAGGCCCTTGACAGGAGCCCTGCGGCAATCC 204

Db 375 AGAGGCTGCCAGCGGGGCACTACTGAAAGGCCCTTGACAGGAGCCCTGCGGCAATCC 434
QY 205 ACCTGCTTGTGTGTGCCCAAGACACCTTTTGGCTGGGAAACACCATATTTCTGAA 264
Db 435 ACCTGCTTGTGTGTGCCCAAGACACCTTTTGGCTGGGAAACACCATATTTCTGAA 494
QY 265 TGTGCCCGCTCCAGAGCCTGTGATGAGCAGGCTTCCAGGTGGCGCTGGAGACTGTTCA 324
Db 495 TGTGCCCGCTCCAGAGCCTGTGATGAGCAGGCTTCCAGGTGGCGCTGGAGACTGTTCA 554
QY 325 GCATGGGCGACACCCGCTGTGGCTGTAAAGCAGGCTGGTTTGGAGTGGCAGGTGAGC 384
Db 555 GCATGGGCGACACCCGCTGTGGCTGTAAAGCAGGCTGGTTTGGAGTGGCAGGTGAGC 614
QY 385 CAATGTGCACAGTTCACCTTCTACTGCAACCATCCTAGACTGGGCGGCTCTGCAC 444
Db 615 CAATGTGCACAGTTCACCTTCTACTGCAACCATCCTAGACTGGGCGGCTCTGCAC 674
QY 445 CGCCACACAGGCTACTGTTCCTCCGAGAGTACTGACTGTGGACTGCTGCTGCGC 504
Db 675 CGCCACACAGGCTACTGTTCCTCCGAGAGTACTGACTGTGGACTGCTGCTGCGC 734
QY 505 TTCTATGAACATGGGATGGCTGCGCTGTCCGCCAGAGACCCGAGAGCCTGGAGCTGTCCA 564
Db 735 TTCTATGAACATGGGATGGCTGCGCTGTCCGCCAGAGACCCGAGAGCCTGGAGCTGTCCA 794
QY 565 GAGCGCTGTGCGCTGTGTGGCTGGAGGCGAGATGTTCTGGGTCCAGTGTCTCTGCT 624
Db 795 GAGCGCTGTGCGCTGTGTGGCTGGAGGCGAGATGTTCTGGGTCCAGTGTCTCTGCT 854
QY 625 GGCCTTGTGGTCCCTCTCTCTGTGGGGCCACCTGACCTACATATACCGCATCTGTGG 684
Db 855 GGCCTTGTGGTCCCTCTCTCTGTGGGGCCACCTGACCTACATATACCGCATCTGTGG 914
QY 685 COTCAAGGCCCTGTGTTACTGACATGATGGATGGAGTGGAGTGGTACCCTCACACCG 744
Db 915 COTCAAGGCCCTGTGTTACTGACATGATGGATGGAGTGGAGTGGTACCCTCACACCG 974
QY 745 GCCACCATCTGTCACTTGTGAGACGCGCCACACCTTCTAGACCTTCTAGACAGCACT 804
Db 975 GCCACCATCTGTCACTTGTGAGACGCGCCACACCTTCTAGACCTTCTAGACAGCACT 1034
QY 805 GAGAAGATGTGACCGCTGACAGTTGGTGTGTAACAGCTGACACCTTGGTACCCCGAGACC 864
Db 1035 GAGAAGATGTGACCGCTGACAGTTGGTGTGTAACAGCTGACACCTTGGTACCCCGAGACC 1094
QY 865 CAGGAGGCGCTGTGCCCGCAGAGTGAATGCTCTGGGACAGTTGCCAGAGACTCTT 924
Db 1095 CAGGAGGCGCTGTGCCCGCAGAGTGAATGCTCTGGGACAGTTGCCAGAGACTCTT 1154
QY 925 GGCCTCGCTGTGCGGCCACTCTTCCAGAGTCCCGAGGCGCTGCCAGCATGATG 984
Db 1155 GGCCTCGCTGTGCGGCCACTCTTCCAGAGTCCCGAGGCGCTGCCAGCATGATG 1214
QY 985 CTGCAAGCGGGGCCGAGCTTACGACGTGATGAGACGGGTCCAGCGGGCGCTGGAG 1044
Db 1215 CTGCAAGCGGGGCCGAGCTTACGACGTGATGAGACGGGTCCAGCGGGCGCTGGAG 1274
QY 1045 GAGTTGCTGCAGCGCTGGGGCTGCGCGAGGCGAGAGATGAAAGCCCTGGAGTGGAGATC 1104
Db 1275 GAGTTGCTGCAGCGCTGGGGCTGCGCGAGGCGAGAGATGAAAGCCCTGGAGTGGAGATC 1334
QY 1105 GGCCTGCTCCGAGACGAGCAGTACGAGATGCTTACGCGCTGGCGCGCAGACACCGCGG 1164
Db 1335 GGCCTGCTCCGAGACGAGCAGTACGAGATGCTTACGCGCTGGCGCGCAGACACCGCGG 1394
QY 1165 GGCCTGAGAGCGTTTACGCGCGCTGAGAGCGATGGGCTGGAGCGCTGCGTGAAGAC 1224
Db 1395 GGCCTGAGAGCGTTTACGCGCGCTGAGAGCGATGGGCTGGAGCGCTGCGTGAAGAC 1454
QY 1225 TTGGCGACGCGCTGACGCGCGCGCTGGA 1254
Db 1455 TTGGCGACGCGCTGACGCGCGCGCTGGA 1484

D	b		1248	CACGCTGGAGACTGTCTGGAGACCGTGCTCCGCCGCATGCACTTCCTTGGCT	1297
R	E	S	I	O	
I	D		020973	standard; DNA: 2062 BP.	
A	C		Q20973;	TNF- α binding protein gene.	
D	T		11-MAY-1992	(first entry)	
D	E		Tumor necrosis factor alpha;	autoimmune diseases; cachectin; ss,	
K	M		extracellular domain.		
K	M		Homo sapiens.		
F	H		Key	Location/Qualifiers	
F	H		cds	155..1522	
F	T		*tag= "a"	/tag= "a"	
F	T		signal_peptide	155..274	
F	T		*tag= "b"	/tag= "b"	
F	T		mat_peptide	275..1522	
F	T		*tag= "c"	/tag= "c"	
F	T		misc_feature	473..532	
F	T		*tag= "d"	/tag= "d"	
F	T		misc_feature	242..751	
F	T		*tag= "e"	/tag= "e"	
F	T		Note= "encodes the extracellular domain of human TNF alpha receptor."		
P	N		GB2246569-A.		
P	D		05-FEB-1992.		
P	F		15-JUN-1990:	013410.	
P	R		15-JUN-1990:	GB-013410.	
P	A		(CHAR-) CHARING CROSS SUNLE.		
P	I		Feldman M, Gray P, Turner M, Brennan F;		
D	R		WPI: 92-043613/06.		
D	R		P-PDSB: R20787.		
P	T		New tumour necrosis factor alpha binding protein and polypeptide useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis		
P	T		- disclosure; Fig 1: 25pp; English.		
P	S		The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obt. from a human placental cDNA library in lambda gtl using a probe (Q20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also Q20974.		
S	Q		Sequence 2062 BP; 429 A; 429 A; 616 C; 573 G; 444 T;		
Q	U	e	r	y	m
B	e	s	t	L	a
.	M	a	t	c	h
.	M	a	t	c	h
Q	Y		996 CCCGACGCTTTACGACGCGATGAGCAGCGGTCGCCAGCGCGCGCGCTGGAMAGAATTGTCGC	1055	
D	b		1222 CGCGACGCTGTAAGCGCGTAGTGGAACAACCTGCCCGCTTGCCTGGAAAGAATTGTCGC	1281	
Q	Y		1056 CACGCTGGGGGCGCGCGAGCGAGCATGGAACC GGAGCGTGAGATGGCGGCTTCGC	1115	
D	b		1282 GCgcctTaagGcttaacgAcgaCcagaAttgatggcggtGaAgaaCGsgcgttccg	1341	
Q	Y		1116 AGACAGCAGTAGTACGAGATGCTCACGCGTGCGCCAGCAGCAGCCCCGGCGGCTTCGGAC	1175	
D	b		1342 GCCGAGGCGCAATAACAGATGCTGGCGACCTGGAGAGCGCGCGCGCGCGAGGC	1401	
Q	Y		1176 CGTTAACGCGCCCCTGGAGCGCATGGGCTGGAGCGGCTtcgTGAAGACT	1225	
D	b		1402 CACGCTGGAGCTGTGGGACGCGCTCCTCCGACATGACCTGTGGGCT	1451	
R	E	S	I	O	
I	D		024440	standard; DNA: 2062 BP.	
A	C		Q24440;		

Query Match	5.3%	Score 66.8	DB 1	Length 2062
Best Local Similarity	55.7%	Pred. No. 4.1e-06		
Matches 128	Conservative 0	Mismatches 102	Indels 0	Gaps 0
0Y	996	CCCCAGGCTCTTCACGAGCATGATGAGCGCGGTCCAGCGCGGCGCCCTGGAGAGATTGCTGCG	1055	
Db	1222	CGCGACGCTGTACGCGCGGTGTGGAGAACACTGTCGCCCGTTGGCCCTGGAAAGAAATTGCTGCG	1281	
0Y	1056	CACGCTGTGGGCTGCGCAGGCGAGAGATCGAAACCGCTGGAGAGTGGAGATCGCCGCTTCGC	1115	
Db	1282	GGCGCTAGGCGGTGACGACACAGAGATGATGCGTGGAGGTGCGAAGACGGCGCTGCT	1341	
0Y	1116	AGACCAAGCATACGAGATGCTTAACGCTGGCGCCAGCAGACAGACCCGGCGGCTTGGAGC	1175	
Db	1342	GGCGAAGCGCATACACATGCTTGGCGACCTGGAGGGGGGCGCCACGCCCGCGGAGGC	1401	
0Y	1176	CGTTTACGCGGCGCTGAGAGCGCATGGGCGTGGAGCGGCTGCGTGGAAAGCT	1225	

DB 1402 CACGCTGAGCTGCTGGAGCGCTGCTCCGCGACATGAGCTGCTGGGCT 1451

RESULT 12

ID 010883 standard; cDNA; 2088 BP.

AC 010883;

DT 13-MAY-1991 (first entry)

DE 30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.

KM Tumour necrosis factor; inhibitor; ss.

OS Homo sapiens.

EH Key

FT Location/Qualifiers

FT cds 171..1536

FT /*tag= a

PN A09058976-A.

PD 24-JAN-1991.

PF 16-JUL-1990; 058976.

PR 18-JUL-1989; US-381080.

PR 11-DEC-1989; US-450329.

PR 07-FEB-1990; US-479661.

PA (SYNE-) SYNEMGEN INC.

DR WPI; 91-073847/11.

DR P-PSDB; R10986.

PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha

PT and -beta, useful as therapeutic agent.

PS Disclosure; Fig 21; 142pp; English.

CC The sequence encodes the entire 30 kD TNF inhibitor. The clone from

CC which the sequence was obt'd. was isolated from a cDNA library

CC prep'd. from RNA form 0937 cells treated with PMA/PHA. The whole

CC gene can be inserted into expression vectors for prep'n. of TNF

CC inhibitor for use in the treatment of inflammatory and degenerative

CC diseases.

CC See also 010878, 010884 and 010907.

SQ Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;

Query Match 5.3%; Score 66.8; DB 1; Length 2088;

Best Local Similarity 55.7%; Pred. No. 4.1e-06;

Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 996 CCCCAGCTCTACGACGTGATGAGACGGGCTCCAGCGCGGCTGGAAGAGTTGCTGCG 1055

DB 1236 CCGCAGCGCTGACCGCGCTGGTGGAGAAAGTCCCGCTGGCGTGAAGAAATTGCTGCG 1295

QY 1056 CAGCGCTGGGGCTGGCGAGGAGAGATGAGAGCCGCTGAGAGTGGCGCGCTTCCG 1115

DB 1296 GCGCTTAGGGCTGAGCGACCGACGAGATGATCGCTGGAAGCTGCAAGAGGGCGCTGCT 1355

QY 1116 AGACGACGAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTTGGAGC 1175

DB 1356 GCGGAGGCGGCAATACAGCATGCTGGGCACTGGAGGCGGCGCACGCGGCGGAGAGC 1415

QY 1176 CGTTAGCGGCGCTGGAGCGCATGGGCTGAGCGGCTGCGTGGAAAGACT 1225

DB 1416 CACGCTGAGAGCTGCTGGGACGCTGCTCCGCGACATGAGACCTGCTGGGCT 1465

RESULT 13

ID 010955 standard; cDNA; 2111 BP.

AC 010955;

DT 24-MAY-1991 (first entry)

DE Encodes human 55kD TNF-binding protein.

KM Tumour Necrosis Factor; binding proteins; septic shock;

KW autoimmune glomerulonephritis; lymphokine; cytokine.

EH Key

FT Location/Qualifiers

FT signal_peptide 187..273

FT /*tag= a

FT mat_peptide 274..1551

FT /*tag= b

FT /product= 55kD TNF-BP

PN EP-417563-A.

PD 20-MAR-1991.

PF 31-AUG-1990; 116707.

PR 12-SEP-1989; CH-003319.

PR 08-MAR-1990; CH-000746.

PR 20-APR-1990; CH-001347.

PA (HOFF) HOFFMANN-LA ROCHE AG.

PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;

PI Schlaeger EJ;

DR WPI; 91-081851/12.

DR P-PSDB; R11082.

PT Insoluble tumour necrosis factor binding proteins - and DNA

PT encoding them, useful in pharmaceutical prods. and for antibody

PT prodn.

PS Claim 4; Fig 1; 26pp; German.

CC Partial amino acid sequences were determined for the 55 and 75kD

CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were

CC synthesised based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human

CC placental cDNA bank constructed in lambda g111. Positive clones were

CC identified and sequenced. DNA constructs comprising the TNF-BP coding

CC sequence may also contain a fragment encoding a human Ig domain.

CC Recombinant constructs are used to transform cells to confer

CC improved TNF-binding properties.

CC See also 010956.

SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

Query Match 5.3%; Score 66.8; DB 1; Length 2111;

Best Local Similarity 55.7%; Pred. No. 4.1e-06;

Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 996 CCCCAGCTCTACGACGTGATGAGACCGGCTCCAGCGCGGCTGGAAGAGTTGCTGCG 1055

DB 1254 CCGCAGCGCTGACCGCGCTGGTGGAGAAAGTCCCGCTGGCGTGAAGAAATTGCTGCG 1313

QY 1056 CAGCGCTGGGGCTGGCGAGGAGAGATGAGAGCCGCTGAGAGTGGCGCGCTTCCG 1115

DB 1314 GCGCTTAGGGCTGAGGAGGACGACGATGATGCGCTGGAGCTGCACAAAGGGCGCTGCT 1373

QY 1116 AGACGACGAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTTGGAGC 1175

DB 1374 GCGGAGGCGGCAATACAGCATGCTGGCGACCTGGAGCGGCGGAGCGCGCGGAGAGC 1433

QY 1176 CGTTAGCGGCGCTGGAGCGCATGGGCTGAGCGGCTGCGTGGAAAGACT 1225

DB 1434 CACGCTGAGAGCTGCTGGGACGCTGCTCCGCGACATGAGACCTGCTGGGCT 1483

RESULT 14

ID 006285 standard; DNA; 2141 BP.

AC 006285;

DT 29-JAN-1991 (first entry)

DE Human Tumour Necrosis Factor-Receptor cDNA insert.

KM Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

KW lambdaTNF-R2; ratTNF-R8; ss.

OS Homo sapiens.

EH Key

FT Location/Qualifiers

FT cds 213..1577

FT /*tag= a

FT /label=huTNF-R

PN EP-393438-A.

PD 24-OCT-1990.

PF 06-APR-1990; 106624.

PR 21-APR-1989; DE-913101.

PR 21-JUN-1989; DE-920282.

PA (BOEH) BOEHRINGER INGELHEIMINT.

PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratawa C;

DR WPI; 90-321987/43.

DR P-PSDB; R07451.

PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action

PS Disclosure; Fig 91(1-2); 51pp; German.

CC ratTNF-R8 (006284) was used to screen the HS913T cDNA library.

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 05:24:33 ; Search time 50.22 seconds
(without alignments)
3434.787 Million cell updates/sec

Title: US-09-314-889-3
Perfect score: 1254
Sequence: 1 ATGGACGACGGCGCGCGGGG.....GCCTGCACGCGCGCGCGTGA 1254

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/5_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.8	5.3	2062	1	US-08-050-319B-24
2	66.8	5.3	2062	3	US-08-465-982-24
3	66.8	5.3	2161	5	US-09-106-038A-1
4	66.8	5.3	2175	1	US-08-321-668-1
5	66.8	5.3	2175	2	US-08-837-941-1
6	66.8	5.3	2175	1	US-08-126-016-1
7	58.8	4.7	1956	4	US-08-762-308-10
8	48.8	3.9	20235	2	US-07-642-734C-3
9	47.2	3.8	1642	1	US-08-232-015-2
10	44.8	3.6	8051	4	US-08-576-626A-2
11	44.6	3.6	2889	2	US-08-537-002A-4
12	44.6	3.6	3600	2	US-08-537-002A-5
13	43.4	3.5	330	1	US-07-849-389-6
14	43	3.4	1931	4	US-09-130-114-2
15	43	3.4	4257	3	US-08-690-473-1
16	43	3.4	12001	2	US-08-458-568A-11
17	42.4	3.4	396	1	US-07-924-063A-4
18	42.4	3.4	660	4	US-08-726-306A-28
19	42.4	3.4	1157	1	US-07-709-949-1
20	42.4	3.4	4524	3	US-08-845-998-7
21	42	3.3	43280	3	US-08-804-227C-1
22	41	3.3	1312	1	US-08-205-506A-1
23	41	3.3	1312	6	PCT-US94-02389-1
24	41	3.3	2793	2	US-08-209-747-1
25	41	3.3	2793	2	US-08-458-298-1
26	40	3.2	204	1	US-07-696-051B-2

c	27	40	3.2	204	1	US-07-924-063A-2	Sequence 2, Appl
	28	40	3.2	4287	1	US-08-244-189-1	Sequence 1, Appl
	29	40	3.2	4287	2	US-08-306-651B-53	Sequence 53, Appl
	30	39.8	3.2	2338	2	US-08-425-069-1	Sequence 1, Appl
	31	39.8	3.2	2338	4	US-08-317-844B-1	Sequence 1, Appl
	32	39.6	3.2	1780	4	US-08-933-821-5	Sequence 5, Appl
	33	39.6	3.2	1780	5	US-08-960-507-5	Sequence 5, Appl
	34	39.2	3.1	28804	3	US-08-597-874-1	Sequence 1, Appl
	35	39.2	3.1	28804	5	US-09-096-942-2	Sequence 2, Appl
	36	39	3.1	1288	2	US-08-440-856A-9	Sequence 9, Appl
	37	39	3.1	20235	2	US-07-642-734C-3	Sequence 116, App
	38	38.8	3.1	927	4	US-08-997-080-116	Sequence 116, App
	39	38.8	3.1	927	4	US-08-997-362-116	Sequence 116, App
	40	38.8	3.1	985	4	US-08-997-080-161	Sequence 161, App
	41	38.8	3.1	985	4	US-08-997-362-161	Sequence 161, App
	42	38.8	3.1	1569	4	US-08-997-080-113	Sequence 113, App
	43	38.8	3.1	1569	4	US-08-997-362-113	Sequence 113, App
	44	38.8	3.1	1626	4	US-08-997-080-159	Sequence 159, App
	45	38.8	3.1	1626	4	US-08-997-362-159	Sequence 159, App

ALIGNMENTS

RESULT 1
US-08-050-319B-24
Sequence 24, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
TITLE OF INVENTION: Modified human TNFalpha (Tumor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..1519
US-08-050-319B-24

Query Match 5.3%; Score 66.8; DB 1; Length 2062;
Best Local Similarity 55.7%; Pred. No. 5.4e-07;
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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Oy	1056	CACGCTGGGGGCTGCGCGAGGCAACAGATCCAGACCGCTGTGAGAGTGAGATCGGCGCCTTCG	1115
Db	1282	GCGGCTAGGGGCTGAGGGGACACAGATCGATCGGCTGTGAACTGCAAGAACGGCGCTGCT	1341
Oy	1116	AGACCAAGCAGTACGAGATGCTCAAGCGCTGGCGCCACAGCAAGCCGCGGGCTCTGGAGC	1175
Db	1342	GCGCGAGGCGCAATACAGATGCTGGCGACCTGGAGCGCGCGCAACGCGCGGCGCCGAGGC	1401
Oy	1176	CGTTTACGGCGGCGCTGAGGCGATGGGGGCTGCGACGCGTGGTGGAGACT	1225
Db	1402	CACGCTGGAAGCTGCTGGAGACGCTGCTCCGCGACATGAGACTCTGTGGGCT	1451

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1      RESULT      2
2      US-08      465-982-24
3      : Sequence 24, Application US/08465982
4      Patent No. 3603786
5      GENERAL INFORMATION:
6      APPLICANT: M.Feldmann, P.W. Gray,
7      APPLICANT: M.J.C. Turner, F.M Brennan
8      TITLE OF INVENTION: Modified human TNFalpha (Tumor
9      NUMBER OF SEQUENCES: 57
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Reed & Robbins
12     STREET: 635 Bryant Street
13     CITY: Palo Alto
14     STATE: California
15     COUNTRY: USA
16     ZIP: 94301
17
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: Patentin Release #1.0, version #1.25
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/465,982
25     FILING DATE:
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: US/08/050,319
29     FILING DATE: 10-MAY-1993
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Robbins, Roberta L.
32     REGISTRATION NUMBER: 33,208
33     REFERENCE/DOCKET NUMBER: 5150-0030
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: (415) 617-8999
36     TELEFAX: (415) 327-3231
37     INFORMATION FOR SEQ ID NO: 24:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 2062 base pairs
40     TYPE: nucleic acid
41     STRANDEDNESS: double
42     TOPOLOGY: linear
43     MOLECULE TYPE: cDNA to mRNA
44     FEATURE:
45     NAME/KEY: CDS
46     LOCATION: 155..1519
47
48     US-08-465-982-24

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Query Match	5.3%	Score 66.8	DB 3	Length 2062
Best Local Similarity	55.7%	Pred. No. 5.4e-07		
Matches 128	Conservative 0	Mismatches 102	Indels 0	Gaps 0
QY	996	CCCCAGCTTACGACGATGATGAGCGCGGTCCCGACGCGCGCGCTGGAAGAGATTCTGCGC	1055	

Db	1222	CCGACGCGTGTAGCCCGCTGGTGGAGAACTGCCCCCGTTGGCGCTGGAGAAATTCGTGCG	1281
QY	1056	CACGCTGTGGGCGCTGCCGAGGCGAGAGATTCGAAGCCGTGGAGGTGGAGATTCGCGCGCTTCGC	1115
Db	1282	GCGCCTTAGGGCTGTGACGACCAACGATCGATCGGCTGTGAGCTGCAGAAACGGGCGCTGCCT	1341
QY	1116	AGACACAGCATGACGAGATGCTCAAGCGCTGCGGCCACAGCAGCCCCGGGGGCGCTGGAGAC	1175
Db	1342	GCGGAGAGCGCCAAATACAGCATTCCTGGCGACCTGGAGGCGGCGCCAGCGCGCGCGGAGGC	1401
QY	1176	CGTTTAAAGCGGCGCCCTGGAGAGCGATGGGGGCTCGAGGCGCTCGTGGAGAGACT	1225
Db	1402	CACGCTGGAAGCTGCTGGGAGCGCTGCTCCGCGACATGAGACTGCTGGGCT	1451

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1      RESULT      3
2      US-09-106-038A-1
3      ; Sequence 1, Application US/09106038A
4      ; Patent No. 6007995
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Brenda F. Baker and Lex M. Cowser
7      ; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI
8      ; TITLE OF INVENTION: EXPRESSION
9      ; NUMBER OF SEQUENCES: 91
10     ; CORRESPONDENCE ADDRESSES:
11     ; ADDRESSEE: Isis Pharmaceuticals, Inc.
12     ; STREET: 2292 Faraday Avenue
13     ; CITY: Carlsbad
14     ; STATE: CA
15     ; COUNTRY: U.S.A.
16     ; ZIP: 92008
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: Windows NT
21     ; SOFTWARE: Microsoft Word 97
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/09/106.038A
24     ; FILING DATE: June 26, 1998
25     ; CLASSIFICATION: 514
26     ; ATTORNEY/AGENT INFORMATION:
27     ; NAME: Laurel Spear Bernstein
28     ; REGISTRATION NUMBER: 37,280
29     ; REFERENCE/DOCKET NUMBER: PFS-0004
30     ; TELECOMMUNICATION INFORMATION:
31     ; TELEPHONE: (760) 931-9200
32     ; TELEFAX: (760) 603-3820
33     ; INFORMATION FOR SEQ ID NO: 1:
34     ; SEQUENCE CHARACTERISTICS:
35     ; LENGTH: 2161
36     ; TYPE: nucleic acid
37     ; STRANDEDNESS: single
38     ; TOPOLOGY: linear
39     ; US-09-106-038A-1

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[illegible]

Db 1503 CACGCTGAGCTGCTGGAGCGCTGCTCCGCGACATGACCTGCTGGGCT 1552

RESULT 4

US-08-321-668-1
: Sequence 1, Application US/08321668
: Patent No. 5665859
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BRAKEBUSCH, Cord
: APPLICANT: VARPOLOMEYEV, Eugene
: APPLICANT: BATKIN, Michael
: TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
: TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/321,668
: FILING DATE: 12-OCT-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 107268
: FILING DATE: 12-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-13
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2175 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 256..1620
: US-08-321-668-1

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Best Local Similarity 5.3%; Score 66.8; DB 1; Length 2175;
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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QY 1056 CACGCTGGGCTCGCGGAGGAGATCGAAGCCGTGAGAGTGCAGATCGCGCTTCG 1115
Db 1383 GCGGCTAGGCTGACGCGGAGGAGATCGATCGGCTGAGAGTGCAGATCGCGCTTCG 1442
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Db 1443 GCGGAGGCGCCATACGATGCTGCGGACCTGAGAGCGGCGGCGGCGGCGGAGC 1502
QY 1176 CGTTACGCGGCGCTGAGCGCATGGGGCTGAGACGCGCTGCTGGAAGACT 1225

Db 1503 CACGCTGAGCTGCTGGAGCGCTGCTCCGCGACATGACCTGCTGGGCT 1552

RESULT 5

US-08-837-941-1
: Sequence 1, Application US/08837941
: Patent No. 5766917
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BRAKEBUSCH, Cord
: APPLICANT: VARPOLOMEYEV, Eugene
: APPLICANT: BATKIN, Michael
: TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
: TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837,941
: FILING DATE: 28-APR-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/321,668
: FILING DATE: 12-OCT-1994
: APPLICATION NUMBER: IL 107268
: FILING DATE: 12-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-13
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2175 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 256..1620
: US-08-837-941-1

Query Match

Best Local Similarity 5.3%; Score 66.8; DB 2; Length 2175;
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 996 CCCGACGCTTACGAGTGTGATGACGGCGTCCAGCGCGGCTGGAAGATTGTCGCG 1055
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QY 1056 CACGCTGGGCTCGCGGAGGAGATCGAAGCCGTGAGAGTGCAGATCGCGCTTCG 1115
Db 1383 GCGGCTAGGCTGACGCGGAGGAGATCGATCGGCTGAGAGTGCAGATCGCGCTTCG 1442
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RESULT 8
US-07-642-734C-3/C
Sequence 3. Application US/07642734C
Patent No. 5824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: McAlpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: Erythromycin Analogs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952. US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Saccharopolyspora erythraea*
STRAIN: NRRL 238
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US-07-642-734C-3
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Best Local Similarity 46.3%; Pred. No. 0.013;
Matches 199; Conservative 0; Mismatches 227; Indels 4; Gaps 1;
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QY 885 GGTGACATGTCCTGGAGACAGTTGCCAGAGAGCTTTGGCCCGCTGCTGCGCCAC 944
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RESULT 9
US-08-232-015-2/c
; Sequence 2, Application US/08232015
; Patent No. 5650272
; GENERAL INFORMATION:
; APPLICANT: GUESDON, Jean-Luc
; APPLICANT: THIERRY, Dominique
; APPLICANT: VINCENT, Veronique
```

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;; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH HYBRIDIZE
;; TITLE OF INVENTION: SPECIFICALLY WITH BACTERIAL STRAINS OF THE MYCOBACTERIUM
;; TITLE OF INVENTION: AVIUM-INTRACELLULAR COMPLEX
;; NUMBER OF SEQUENCES: 66
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/232,015
;; FILING DATE: 02-MAY-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO 93/09251
;; FILING DATE: 13-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 91/13504
;; FILING DATE: 31-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Crane-Feury, Sharon E
;; REGISTRATION NUMBER: 36,113
;; REFERENCE/DOCKET NUMBER: 004900-127
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1642 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium avium
US-08-232-015-2
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Query Match 3.8%; Score 47.2; DB 1; Length 1642;
Best Local Similarity 48.5%; Pred. No. 0.017;
Matches 130; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
```

```
QY 878 GCCCGAGGTGACATGCTCTGGGACCAAGTTGCCAGAGCTTTGGCCCGCTG 937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 341 GCCCTGGCGGAGATATCCCGGTGACCGGATGACCGGCAATGATCTTCGCGCATG 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 938 CGGCCACATCTTCGCCAGAGTCCCAAGCGGCTCGCCAGCCATGATGCTGCAACCGGGCC 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 GACACACACCGACCCCGGTGCGCTGCGCGGAGATGCGCGGATGCGCAAGTCAATGTC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 998 CGGAGCTTACAGCATGATGAGACGCGTCCACAGCGGCGCTGGAAGAGATTGCTGCGCA 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 CGGGGCGGCTGGCGGAGAGTGGCTTGATCAAGGCGCGGCGGAGATGGGCGGG 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1058 CGCTGGGCTGCGCGAGAGAGATGAAAGCCGTGAGGTGAGATCGGCCCTTCGAG 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 161 CCCAAGCGGTGGCTTGGCGAGAGAGGCGCCGACATCGTGGCGCTGACCTTGGCGAG 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1118 ACCAGCATACAGATGCTCAAGCGCTG 1145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 101 CGGTGACACAGGTATGTTCCGCCAG 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 10
```


Wed Jul 26 07:05:03 2000

us-09-314-889-3.rml

Page 10

Search completed: July 23, 2000, 06:28:45
Job time: 3852 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 05:02:15 ; Search time 466.05 Seconds
(without alignments)
11865.518 Million cell updates/sec

Title: US-09-314-889-3

Perfect score: 1254

Sequence: 1 ATGGAGCAGCGCGCGCGG.....GCCCTGACGCGCGCCCTGCA 1254

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
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10: em_est10:*
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113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*

117: gb-gss13:.*
118: gb-gss14:.*
119: gb-gss15:.*
120: gb-gss16:.*
121: gb-gss17:.*
122: gb-gss18:.*
123: gb-gss19:.*
124: em-gss13:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	665	53.0	698	44	AI807913	AI807913 wf52c03.x
2	591	47.1	632	70	AM268610	AM268610 xv41b12.x
3	582	46.4	688	39	AI424936	AI424936 q19b08.x
4	561	44.7	562	35	AI140043	AI140043 qab7a04.x
5	535.4	42.7	585	73	AM517358	AM517358 xp93g02.x
6	508	40.5	508	36	AI203624	AI203624 qe75f02.x
7	444	35.4	478	62	AM002222	AM002222 wf55c09.x
8	409.4	32.6	422	43	AI700459	AI700459 wd14b11.x
9	353.6	28.2	433	85	H41522	H41522 yn90f12.s1
10	331	26.4	432	87	N71143	N71143 za80h09.s1
11	326.4	26.0	623	44	AI811528	AI811528 tw43h06.x
12	299	23.8	500	27	AA476747	AA476747 zw94b11.x
13	289.6	23.1	345	33	AA934992	AA934992 op33h05.s
14	284.8	22.7	587	38	AI380959	AI380959 tg18c01.x
15	273.2	21.8	372	91	W76376	W76376 zdb6a06.r1
16	270	21.5	322	63	AA971249	AA971249 op73c01.s
17	263	21.0	582	69	AM182875	AM182875 xp99a04.x
18	262.2	20.9	618	63	AM074008	AM074008 xb06c09.x
19	241	19.2	330	87	N71141	N71141 za80g11.s1
20	239	19.1	544	38	AI380900	AI380900 tg17f01.x
21	232.6	18.5	468	86	H46374	H46374 y014h09.r1
22	230.2	18.4	443	86	H46211	H46211 y014h09.r1
23	220.8	17.6	537	37	AI266746	AI266746 q911c06.x
24	194	15.5	316	86	H49675	H49675 y023d06.r1
25	183.8	14.7	393	85	H41851	H41851 y007f03.r1
26	177.4	14.1	397	86	H46378	H46378 y012f05.r1
27	172	13.7	605	46	AI913906	AI913906 wd03f01.x
28	170.2	13.6	739	27	AA524052	AA524052 ng33b06.s
29	163.6	13.0	523	91	W71984	W71984 zdb6a06.s1
30	160.8	12.8	292	21	AA088350	AA088350 z182d08.r
31	151.4	12.1	246	85	AI19739	AI19739 yn60h04.r1
32	150.2	12.0	418	86	H46662	H46662 y012e12.r1
33	149.4	11.9	596	32	AA887388	AA887388 o37a02.s
34	148	11.8	433	64	AM134494	AM134494 ui-H-B11-
35	147.4	11.8	246	86	H46424	H46424 y012e12.s1
36	124	9.9	348	43	AI703436	AI703436 we24c02.x
37	122.8	9.8	151	33	AA954505	AA954505 on81c01.s
38	109.8	8.8	437	73	AA492480	AA492480 ui-M-BH3-
39	109.4	8.7	401	21	AA088232	AA088232 z182d08.s
40	99.4	7.9	201	85	H22502	H22502 yn69g06.r1
41	98	7.8	378	29	AA631757	AA631757 np76c04.x
42	70.2	5.6	392	37	AI300222	AI300222 gm70c06.x
43	66.4	5.3	925	122	CNS0091P	AL053013 Drosophila
44	63.6	5.1	203	87	N55389	N55389 yz18c11.r1
45	62.8	5.0	562	26	AA460610	AA460610 zx62a05.r

ALIGNMENTS

RESULT 1
LOCUS AI807913 698 bp mRNA
DEFINITION wf52c03.x1 Soares.NFL.T_GBC.S1 Homo sapiens cDNA clone
IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN

PRECUSOR :, mRNA sequence.
ACCESSION AI807913
VERSION AI807913.1 GI:5394479
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 698)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL On Apr 7, 1998 this sequence version replaced g1:3035738.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.L.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1568 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 459.

FEATURES

source
1..698
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2359204"
/clone.lib="Soares.NFL.T_GBC.S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site:1 Not I; Site:2 Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19w, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT

111 a 218 c 214 g 155 t

Query Match 53.0%; Score 665; DB 44; Length 698;
Best Local Similarity 97.1%; Pred. No. 9.5e-140;
Matches 677; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

38 CGGCGCTCTCTGCTGCTGCTGGGGCGCCGACAGGCGGACCTGTAGCCCGAGT 97
|||||
1 CGGCGCTCTCTCTGCTGCTGCTGGGGCGCCGACAGGCGGCGCTGTATCCCGAGT 60
|||||
98 GTGACTGTGCGCGGTGACTTCCACAGAGATTGCTGTTTGTTCAGAGGCTGCCAG 157
|||||
61 GTGACTGTGCGCGGTGACTTCCACAGAGATTGCTGTTTGTTCAGAGGCTGCCAG 120
|||||
158 CGGCGCTCTCTGAGGCGCCCTTCACAGAGCGCTGGGCGCACTCCACTGCTTGT 217
|||||
121 CGGCGCTCTCTGAGGCGCCCTTCACAGAGCGCTGGGCGCACTCCACTGCTTGT 180
|||||
218 GTCCCCAGACACCTTCTGGCTGGGAGACACCATTAATCTGAATGTGCCGCTGCC 277
|||||
181 GTCCCCAGACACCTTCTGGCTGGGAGACACCATTAATCTGAATGTGCCGCTGCC 240
|||||
278 AGGCTGTGATGAGCAGGCGCTCCAGTGGCGCTGGAGACTGTTTCAGAGTGGCGGACA 337
|||||
241 AGGCTGTGATGAGCAGGCGCTCCAGTGGCGCTGGAGACTGTTTCAGAGTGGCGGACA 300
|||||
338 CGGCGCTGTGCTGTAAAGCAGGCTGTTTGTGAGATGCCAGTCCAGCCAAATGTGTACGA 397
|||||
301 CGGCGCTGTGCTGTAAAGCAGGCTGTTTGTGAGATGCCAGTCCAGCCAAATGTGTACGA 360
|||||

QY 398 GTTCACCCCTTCTACTGCAACCATGCTAGACTGCGGGCCCTGCACCGCCACACGCG 457
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Db 361 GTTCACCCCTTCTACTGCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACGCG 420
QY 458 TACTCTGTTCCCGACAGATAGTACTGTGGAGCTGCGCTGCGCTTCTATGACATG 517
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Db 421 TACTCTGTTCCCGACAGATAGTACTGTGGAGCTGCGCTGCGCTTCTATGACATG 480
QY 518 GGGATGGCGGCTGCTGCTGCGCCACGACGCGCTGGGAGCTGTCAGACGCGCTGCCG 577
|||||
Db 481 GGGATGGCGGCTGCTGCTGCGCCACGACGCGCTGGGAGCTGTCAGACGCGCTGCCG 540
QY 578 CTGTCTGTGGCTGAGAGCATGTCTGTGGTCCAGGTGCTGCTGCGCGCTTGTGTC 637
|||||
Db 541 CTGTCTGTGGCTGAGAGCATGTCTGTGGTCCAGGTGCTGCTGCGCTTGTGTC 600
QY 638 CCCTCTGCTTGGGGCCACCGCTGACCTACACATACCGGCACTGCTGCGTCACAGCCG 697
|||||
Db 601 CCCTCTGCTTGGGGCCACCGCTGACCTACACATACCGGCACTGCTGCGTCACAGCCG 660
QY 698 TGGTACGACATGAAGCTGGGATGAGGCTCTGAC 734
|||||
Db 661 CTGTACTGCAATGAAGCTGGGATGAGGCTCTGAC 697

RESULT 2

AM268610

LOCUS

AM268610 632 bp mRNA EST 03-JAN-2000
xv41b12.x1 Soares.NFL.T_GBC.S1 Homo sapiens cDNA clone
IMAGE:2815679.3', similar to SW:WSL_HUMAN 093038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.

ACCESSION

AM268610

VERSION

EST.

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 632)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jul 7, 1999 this sequence version replaced gi:5866115.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 455.

FEATURES

source

1. 632

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2815679"

/clone_1lb="Soares.NFL.T_GBC.S1"

/lab_host="DH10B"

/note="organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NbH19w, testis NHT, and B-cell

NCI-CGAP-GCH1) were mixed, and ss clones were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

1.M.A.G.E. clones 297480-302087, 682632-687233,

726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo.

BASE COUNT 102 a 194 c 192 g 143 t 1 others

ORIGIN

Query Match

Best Local Similarity 47.18; Score 591; DB 70; Length 632;

Matches 606; Conservative 0; Mismatches 26; Indels 0; gaps 0;

QY 47 TTCGTGTCCTGCTGGGGGCGGGGCGGCGGCGGCACTGTAAGCCCGAGGTGTGACTGTG 106
|||||
Db 1 TCTGTGTCTCTGAGGGGCGGGGCGGCGGCGGCACTGTAAGCCCGAGGTGTGACTGTG 60
QY 107 CCGGTGACTTCCACAGAAGATGTTGCTGTTTGTGTCAGAGGCTGCCAGGGGGCACT 166
|||||
Db 61 CCGGTGACTTCCACAGAAGATGTTGCTGTTTGTGTCAGAGGCTGCCAGGGGGCACT 120
QY 167 ACTGAAGGCCCTTTCAGAGAGCCCTGCGGCACTCCACTGCTTGTGTGCCAAG 226
|||||
Db 121 ACTGAAGGCCCTTTCAGAGAGCCCTGCGGCACTCCACTGCTTGTGTGCCAAG 180
QY 227 ACACCTCTTGGGCTGGGAGAACCACTAATTTCTGAATGTGCCGCTGCCAGGCTGTG 286
|||||
Db 181 ACACCTCTTGGGCTGGGAGAACCACTAATTTCTGAATGTGCCGCTGCCAGGCTGTG 240
QY 287 ATGAGCAGGCTCCAGAGTGGCGCTGAGAACTGTTTCAGAGTGGCGGACACCGGCTGTG 346
|||||
Db 241 ATGAGCAGGCTCCAGAGTGGCGCTGAGAACTGTTTCAGAGTGGCGGACACCGGCTGTG 300
QY 347 GCTGTAAAGCAGGCTGTTGTGTGAGTCCAGGTCCAGGCAATGTGTACAGAGTTACCT 406
|||||
Db 301 GCTGTAAAGCAGGCTGTTGTGTGAGTCCAGGTCCAGGCAATGTGTACAGAGTTACCT 360
QY 407 TCTACTGCAACCATGCTTACAGTGGGGGCGGCGGCGGCACTGCTTATGAAATGCGATGCT 466
|||||
Db 361 TCTACTGCAACCATGCTTACAGTGGGGGCGGCGGCGGCACTGCTTATGAAATGCGATGCT 420
QY 467 CCGGACAGATAGTACTGTTGGGACCTGCTGCGCTGCTTATGAAATGCGATGCTGCT 526
|||||
Db 421 CCGGACAGATAGTACTGTTGGGACCTGCTGCGCTGCTTATGAAATGCGATGCTGCT 480
QY 527 GCGTGTCTGCTGGCCACGACGACCGCTGGGGAGCTGTCCAGAGCGCTGTCGCTGTG 586
|||||
Db 481 GTGTGTCTGCTGGCCACGACGACCGCTGGGGAGCTGTCCAGAGCGCTGTCGCTGTG 540
QY 587 GCTGGAGGCAATGTTCTGGGTTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 646
|||||
Db 541 GCTGGAGGCAATGTTCTGGGTTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 647 TTGGGGCCACCGCTGACCTACACATACCGGCGAC 678
|||||
Db 601 TTGGAGGCATCTTGAACATACTGTCCAC 632

RESULT 3
A1424936 688 bp mRNA EST 30-MAR-1999
LOCUS A1424936
DEFINITION t919b08.x1 NCI-CGAP-CL11 Homo sapiens cDNA clone IMAGE:2109207 3',
similar to TR:000276 000276 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
2. ;, mRNA sequence.
ACCESSION A1424936
VERSION A1424936.1 GI:4270854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

|||||
Db 181 GCCCTGGCGCAACTCCACCTGCTTGTGTGTCCCAAGACACCTTCTTGGCTGGAGAA 240
QY 249 CCACATTAATTTGTAATGTGCCCCCTGCGAGCCTGTGATAGACAGCCTCCAGGTGGC 308
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Db 241 CCACATTAATTTGTAATGTGCCCCCTGCGAGCCTGTGATAGACAGCCTCCAGGTGGC 300
QY 309 GCTGGAATGCTTTTACACAGTGGCGGACACCGGCTGTGGCTGTAAAGCAGGCTGGTTGT 368
|||||
Db 301 GCTGGAGAACTGTTTACACAGTGGCGGACACCGGCTGTGGCTGTAAAGCAGGCTGGTTGT 360
QY 369 GGAATGCGAGGTACGCCAATGTGTACACAGTTCAACCTTTACTTACTGCCAATGCTTGA 428
|||||
Db 361 GGAATGCGAGGTACGCCAATGTGTACACAGTTCAACCTTTACTTACTGCCAATGCTTGA 420
QY 429 CTGGGGGGGGCTGACCGCGCACACAGGCTTACTGTTCCTCCGACAGACTACTGACTGG 488
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Db 421 CTGGGGGGGGCTGACCGCGCACACAGGCTTACTGTTCCTCCGACAGACTACTGACTGG 480
QY 489 GACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCTCCGACGAGAGCAG 548
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Db 481 GACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCTCCGACGAGAGCAG 540
QY 549 CCGGGGAGCTGTCCAGAGCGC 570
|||||
Db 541 CCGNGAGAGCTGTCCAGAGCGC 562
RESULT 5
AM517358 585 bp mRNA EST 03-MAR-2000
LOCUS xp93402.x1 Soares_NHCE-cervix Homo sapiens cDNA clone IMAGE:2747954
DEFINITION 3' similar to TR:000276 000276 LYMPHOCTE ASSOCIATED RECEPTOR OF
DEATH 2.; mRNA sequence.
AM517358
VERSION AM517358.1 GI:7155440
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 585)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 489.
Location/Qualifiers
1.585
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2747954"
/clone_lib="Soares_NHCE-cervix"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pRTT3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - c1190(dT) primer (5'
TGTACCAATCTGACGTGGAGCGCGCGGCTTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonalde."
BASE COUNT 94 a 181 c 193 g 117 t
ORIGIN

Query Match 42.7%; Score 535.4; DB 73; Length 585;
Best Local Similarity 98.9%; Pred. No. 1.3e-110;
Matches 539; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 9 GCGCGCGGGGCTGCGGGGCGGGGCGGCTCCCTCGTGTCTCTGGGGGCGCG 68
|||||
Db 1 GCGGCGCGGGGCTGCGGGGCGGGGCGGCTCCCTCTCTGTGTCTGTGGGGCGCG 60
QY 69 GCGCGAGGGCGGCACTGCTAGCCCGAGGTGTACTGTGCGGGTGCATTCACAGAAAT 128
|||||
Db 61 GCGCCAGGGGCGGCACTGCTAGCCCGAGGTGTACTGTGCGGGTGCATTCACAGAAAT 120
QY 129 TGGTCTGTTTGTTCAGAGGCTGCCACGCGGGGCACTACCTGAAGGCCCTTGCACGA 188
Db 121 TGGTCTGTTTGTTCAGAGGCTGCCACGCGGGGCACTACCTGAAGGCCCTTGCACGA 180
QY 189 GCGCTGCGGCAATCCACCTGCTGTGTGTCCCAAGACACTTCTTGGCGGAGAA 248
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Db 181 GCGCTGCGGCAATCCACCTGCTGTGTGTCCCAAGACACTTCTTGGCGGAGAA 240
QY 249 CCACATTAATTTGTAATGTGCCCCCTGCGAGCCTGTGATAGACAGCCTCCAGGTGGC 308
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Db 241 CCACATTAATTTGTAATGTGCCCCCTGCGAGCCTGTGATAGACAGCCTCCAGGTGGC 300
QY 309 GCTGGAATCTTGTGACAGTGGCGGACACCGGCTGTGTGCTTAAAGCAGGCTGTTTGT 368
Db 301 GCTGGAATCTTGTGACAGTGGCGGACACCGGCTGTGTGCTTAAAGCAGGCTGTTTGT 360
QY 369 GGAGTGGCAGGTACGCCAATGTGTGACAGTTCACCTTCTTCTGCAACCAATGGCTAGA 428
Db 361 GGAGTGGCAGGTACGCCAATGTGTGACAGTTCACCTTCTTCTGCAACCAATGGCTAGA 420
QY 429 CTGGGGGGGGCTGACCGCGCACACAGGCTTACTGTTCCCGACAGACTACTGACTGG 488
Db 421 CTGGGGGGGGCTGACCGCGCACACAGGCTTACTGTTCCCGACAGACTACTGACTGG 480
QY 489 GACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCTCCGACGAGAGCAG 548
Db 481 GACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCTCCGACGAGAAAT 540
QY 549 CCGG 553
Db 541 CCGAG 545
RESULT 6
AI203624 508 bp mRNA EST 29-OCT-1998
LOCUS AI203624
DEFINITION ge/5f02.x1 Soares_fetal_lung_NBH119W Homo sapiens cDNA clone
IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR; mRNA sequence.
AI203624
VERSION AI203624.1 GI:3756230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 508)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 442.

[illegible]

QY	249	CCACCATATTTTGTGATGTGTGCCCGCTGCCAGGCGCTGTGATGACGACGAGCTCCACAGGTGC	308
Db	241	CCACCATATTTTGTGATGTGTGCCCGCTGCCAGGCGCTGTGATGACGACGAGCTCCACAGGTGC	300
QY	309	GCTGAGAACTGTTCAGCATGTGCGCACACCCGCTGGCTGTAAAGCAGAGCTGGTTGT	368
Db	301	GCTGAGAACTGTTCAGCATGTGCGCACACCCGCTGGCTGTAAAGCAGAGCTGGTTG-	359
QY	369	GGAGTCCAGGTCACGCAATGTGTGACGAGTTACCCCTTCTACTGCCCACATGCTTGA	428
Db	360	GGAGTCCAGGTCACGCAATGTGTGACGAGTTACCCCTTCTACTGCCCACATGCTTGA	419
QY	429	CTG 431	
Db	420	CTG 422	
RESULT	9		
LOCUS	H41522	433 bp	MRNA
DEFINITION	yn90f12.s1 Soares adult brain N2b5HB55Y	Homo sapiens	CDNA clone
ACCESSION	H41522		
VERSION	H41522.1	GI:917574	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 433) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P., and Wilson, R.		
TITLE	The Mashu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	On Dec. 20, 1995 this sequence version replaced gi:1134270. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 852 High quality sequence stops: 360 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 852 Std Error: 0.00 Seq primer: Promega -21ml3 High quality sequence stop: 360. Location/Qualifiers 1..433 /organism="Homo sapiens" /db_xref="GDB:3837923" /db_xref="taxon:9606" /clone="IMAGE:175727" /clone_lib="Soares adult brain N2b5HB55Y" /sex="Male" /dev_stage="55-year old" /lab_host="DH10B (ampicillin resistant)" /note="Organ: brain; Vector: pRT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTTCTTTT 3'] TGTTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTTCTTTT 3'] adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was		

Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the

7. [2] TR:00279 ; , mRNA sequence.
A1811528

VERSION	AI811528.1	GI:5398094
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	
AUTHORS	1 (bases 1 to 623)	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
	Unpublished (1997)	
JOURNAL	On Oct 6, 1998 this sequence version replaced gi:3709744.	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 2337 Std Error: 0.00 Seq primer: -400P from GlDco High quality sequence stop: 392. Location/Qualifiers 1..623 /organism="Homo sapiens" /db_xref="taxon:9606" /clone IMAGE:2262491" /clone_1db="NCI-CCAP_U1" /tissue_type="Well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab_host="DH10B" /note="Organ: uterus; Vector: pCMV-SPO076; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"	
BASE COUNT	105 a 188 c 199 g 128 t 3 others	
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Query Match	26.0%; Score 326.4; DB 44; Length 623;	
Best Local Similarity	96.0%; Pred. 1.2e-63;	
Matches 333; Conservative 0; Mismatches 14; Indels 0; Gaps 0;		
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Db 622 TGCCAGCAGAGCTTGGCCCCGCTGCTGCGCCGACACTCTGCGCAGAGTCCCGACGCGG 563		
QY 968 GCTGCGCAGCATATGCTGACGCCGGGCCCCGACACTTACGAGCTGATGACGGGGTCC 1027		
Db 562 CTCGCCAGCATATGCTGACGCCGGGCCCCGACACTTACGAGCTGATGMAACGGGTCC 503		
QY 1028 CAGCGCGCGCTGAGAGAGTTCGTGCGCCAGCGTGGGCTCGCGCAGAGCAGAGATCGAAG 1087		
Db 502 CAGCGCGCGCTGAGAGAGTTCGTGCGCCAGCGTGGGCTCGCGCAGAGCAGAGATCGAAG 443		
QY 1088 CCGTGAGAGTGGAGATCGGCGCTTCCGAGACACAGACTAGAGATGCTCAAGCGCTGGC 1147		
Db 442 CCGTGAGAGTGGAGATCGGCGCTTCCGAGACACAGACTAGAGATGCTCAAGCGCTGGC 383		
QY 1148 GCCAGACACACCCCGGGGCTCTGGAGCGCGTTTACGGGGCTCTGGAGCGCATGGGGCTGG 1207		
Db 382 GCCAGACACACCCCGGGGCTCTGGAGCGCGTTTACGGGGCTCTGGAGCGCATGGGGCTGG 323		
QY 1208 ACGGCTGGTGAAGACTTGGCAGACCCCTGACAGCGGGCGCCGTGA 1254		
Db 322 ACGGCTGGTGAAGACTTGGCAGACCCCTGACAGCGGGCGCCGTGA 276		

AA476747	LOCUS	AA476747	500 bp	mRNA	EST	08-AUG-1997
AA476747	DEFINITION	zw94b11.1	Scars_total_fetus_ND2HF8_9w	Homo sapiens cDNA clone		
AA476747	IMAGE	784605	5', mRNA sequence.			
AA476747	ACCESSION	AA476747				
AA476747.1	VERSION	GI:2204958				
EST.	KEYWORDS					
human.	SOURCE					
Homo sapiens	ORGANISM					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
1 (bases 1 to 500)	REFERENCE					
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Knabe, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Treising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.	AUTHORS					
Washu-Merck EST Project 1997						
Unpublished (1997)	TITLE					
Contact: Wilson RK	JOURNAL					
Washington University School of Medicine	COMMENT					
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108						
Tel: 314 286 1800						
Fax: 314 286 1810						
Email: est@watson.wustl.edu						
This clone is available royalty-free through LLNL; contact the						
Seq Consortium (info@image.llnl.gov) for further information.						
Seq primer: -28ml3 rev2 ET from Amersham						
High quality sequence stop: 473.						
Location/Qualifiers	FEATURES					
1..500	SOURCE					
/organism="Homo sapiens"						
/db_xref="GDB:5982223"						
/db_xref="taxon:9606"						
/clone="IMAGE:784605"						
/clone_lib="Scars_total_fetus_ND2HF8_9w"						
/dev_stage="8-9 weeks"						
/lab_host="DH10B"						
/note="vector: pT73D-Pac (Pharmacia) with a modified						
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA						
was prepared from mRNA obtained from pooled 8-9 week						
(total) fetus material with a Not I - oligo(dT) primer [5'						
TGTTACCAATCTGAAGTGGAGCGCGCGCTTAATTTTCTTTTCTTTT 3']						
Double-stranded cDNA was ligated to Eco RI adaptors						
(Pharmacia), digested with Not I and cloned into the Not I						
and Eco RI sites of the modified pT73 vector. Library						
went through one round of normalization, and was						
constructed by Bento Soares and M. Fatima Bonaldo."						
BASE COUNT		90 a	158 c	162 g	90 t	
ORIGIN						
Query Match		23.8%	Score 299;	DB 27;	Length 500;	
Best Local Similarity		99.4%	Pred. No. 1.8e-57;			
Matches 321;		Conservative	0;	Mismatches	0;	Indels 2;
						Gaps 2;
599	TGTTCTGGGTCAGAGTGTCTCCGTGGCTGTGTCGTCGTCCTGCTGCTGGGGCCACC	658				
180	TGTTCTGGGTCAGAGTGTCTCCGTGGCTGTGTCGTCGTCCTGCTGCTGGGGCCACC	239				
659	TGACCTACACATATCCGCGACATGTCGCTGTCAACAGCCCTGTTACTGTCAGATGAAGCTG	718				
240	TGACCTACACATATCCGCGACATGTCGCTGTCAACAGCCCTGTTACTGTCAGATGAAGCTG	299				
719	GGATGGAGGCTCTAGACCCGACCGGCGGCGACCCATCTGTACCTTGAGACAGCGCCACA	778				
300	GGATGGAGGCTCTAGACCCGACCGGCGGCGACCCATCTGTACCTTGAGACAGCGCCACA	359				
779	CCCTTCTAGCACCTCTGACAGCAGTAGAGATCTGCACCGCTCCAGTTGGTGGTAACA	838				
360	CCCTTCTAGCACCTCTGACAGCAGTAGAGATCTGCACCGCTCCAGTTGGTGGTAACA	419				
839	GCTGAGCCCTGCGTACCCCGAGACCCAGAGGCGCTTGCCTCCGACGATGATGTCCT	898				

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Db      420  GGTGAACCCCTGGCTACCCGAGACCCAGAGGCGCTCTG-CGCGAGTGCATGTCCT 478
QY      899  GGGACCAAGTTGCCAGCAGAGCT 921
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Db      479  GGGA-CAGTTGCCAGCAGAGCT 500

RESULT 13
AA934992      345 bp      mRNA      EST      07-JUL-1998
LOCUS      op33h05.s1 Soares.NFL.T_GBC_S1 Homo sapiens cDNA clone
DEFINITION  IMAGE:1578681 3' similar to TR:014866 014866 SOLUBLE DEATH RECEPTOR
3 BETA. ; mRNA sequence.
ACCESSION  AA934992
VERSION     AA934992.1 GI:3092204
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 345)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL     Tumor Gene Index
COMMENT     Unpublished (1997)
            On Apr 21, 1998 this sequence version replaced gi:3072128.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            This clone is available royalty-free through LINT; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1648 Std Error: 0.00
            Seq primer: -40m13 fwd. Ej from Amersham
            High quality sequence stop: 131.
            Location/Qualifiers
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              /clone_1lb="Soares.NFL.T_GBC_S1"
              /lab_host="DH10B"
              /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
              a modified polylinker; Site_1: Not I; Site_2: Eco RI;
              Equal amounts of plasmid DNA from three normalized
              libraries (fetal lung NBH19W, testis NHT, and B-cell
              NCI-CGAP-GCB1) were mixed, and ss circles were made in
              vitro. Following HAP purification, this DNA was used as
              tracer in a subtractive hybridization reaction. The driver
              was PCR-amplified cDNAs from pools of 5,000 clones made
              from the same 3 libraries. The pools consisted of
              I.M.A.G.E. clones 297480-302087, 682632-687239,
              726408-728711, and 729096-731399. Subtraction by Bento
              Soares and M. Fatima Bonaldo."
BASE COUNT      56 a      105 c      116 g      68 t
ORIGIN
Query Match      23.1%; Score 289.6; DB 33; Length 345;
Best Local Similarity 96.6%; Pred. No. 2.2e-55;
Matches 317; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Db      28  GCGGTGGCGGGGCGGCTCCTGGTGTGCTGGGGGCGCGCCAGGCGGCACTGCT 87
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Db      15  GCGGTGGCGGGGCGG-CCTCTCTCTGTGCTGCTGGGGGCGCGGCGGCACTGCT 72
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QY      88  AGCCCAAGTGTGACTGTGCGGCGTACTTCCACAAGAAGATTGCTGTTTGTTCAGA 147
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Db      73  AGCCCAAGTGTGACTGTGCGGCGTACTTCCACAAGAAGATTGCTGTTTGTTCAGA 132
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QY      148 GCGTGGCCAGGCGGCACTACTGAAGGCCCTTGACGAGGCGCTGGGGCAACGCCACC 207
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Db      133 GCGTGGCCAGGCGGCACTACTGAAGGCCCTTGACGAGGCGCTGGGGCAACGCCACC 192
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QY      208  TGCCCTGTGTGCCCAAGACACCTTCTTGCCCTGGGAGAACACCAATTAATTCGAATGT 267
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Db      253  GCGCGCTGCCAGGCGCTGTGATGAGCAGGCGCTCCAGGTTGGCGCTGGAGAACGTTCACGA 312
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QY      328  GTGGCCGACACCGCGCTGTGGCTTAAGC 355
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Db      313  GTGGTGCACACCGCGCTGTGGCTTAAGC 340
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LOCUS      tg18c01.x1 NCI-CGAP_C1L1 Homo sapiens cDNA clone IMAGE:2109120 3'
DEFINITION  Similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. (2) TR:000279 ; mRNA sequence.
ACCESSION  A1380959
VERSION     A1380959.1 GI:4190801
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 587)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL     Tumor Gene Index
COMMENT     Unpublished (1997)
            On Oct 8, 1998 this sequence version replaced gi:3730839.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LINT at:
            www.bio.llnl.gov/dbp/ncicgap/ncicgap.html
            Insert Length: 1237 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 325.
            Location/Qualifiers
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              /db_xref="taxon:9606"
              /clone="IMAGE:2109120"
              /clone_1lb="NCI-CGAP_C1L1"
              /tissue_type="B-cell, chronic Lymphocytic Leukemia"
              /lab_host="DH10B"
              /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
              polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
              was primed with a Not I - oligo(dT) primer [5'
              TGTTACCAATCTGAGAGGAGCGCGCCCATGCTGTTTTTTTTTTTTTTTTTTT
              T 3']; double-stranded cDNA was ligated to Eco RI
              adaptors (Pharmacia), digested with Not I and cloned into
              the Not I and Eco RI sites of the modified pT7T3 vector.
              Library is normalized, and was constructed by Bento
              Soares and M. Fatima Bonaldo."
BASE COUNT      99 a      192 c      176 g      120 t
ORIGIN
Query Match      22.7%; Score 284.8; DB 38; Length 587;
Best Local Similarity 94.6%; Pred. No. 2.8e-54;
Matches 295; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      943  ACACCTCTGCCAGAGTCCCGGCTGCGCAGGCATATGCTGAGCGGCGCGGCGAG 1002
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Db 587 ACACCTTTGGCAGAGATCCAGCGGGGCTGCGCAAGCCATGATGTGCAAGCGGGGCCGAC 528
OY 1003 CTCTACGAGATATGAGCCGGTCCAGCGGGCGCTGGAAGAGTTCTGTGGCAGCGTG 1062
Db 527 CTTTACGAGATGATGACCGCTCCCAAGCGCGCGCTGGAAGAGTTCTGTGGCAGCGTG 468
OY 1063 GGGCTGCGCGAGAGATCGAAGCGCGGTGAGGTGAGATGCGCGCTTCGAGACGAC 1122
Db 467 GGGCTGCGCGAGAGATCGAAGCGCGGTGAGGTGAGATGCGCGCTTCGAGACGAC 408
OY 1123 CAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACCGCGCGCTCGAGAGCGTTTAC 1182
Db 407 CAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACCGCGCGCTCGAGAGCGTTTAC 348
OY 1183 GGGCGCTGAGACGATGGCGCTGAGCGGCTGCTGTGAAGACTTGGCGAGCGCGCTGAC 1242
Db 347 GCGGCGCTGAGAGCGATGGGCTGAGCGGCTGCTGTGAAGACTTGGCGAGCGCGCTGAC 288
OY 1243 CGCGCGCGCTGA 1254
Db 287 CGCGCGCGCTGA 276

RESULT 15
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LOCUS zdb6a06.r1 Soares_fetal_heart_NbHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:345386 5', mRNA sequence.
ACCESSION W76376
VERSION W76376.1 GI:1386600
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
On Jan 7, 1998 this sequence version replaced gi:948013.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 969 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 352.
Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="Soares_fetal_heart_NbHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT73p (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of

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normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W.
BASE COUNT 71 a 133 c 106 g 59 t 3 others
ORIGIN
Query Match 21.8%; Score 273.2; DB 91; Length 372;
Best Local Similarity 96.3%; Pred. No. 1.1e-51;
Matches 342; Conservative 0; Mismatches 6; Indels 7; Gaps 6;
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Db 7 CCTGTGTTACTGCAATGAAAGCTGGATGAGGCTGTGACCCGACCCGACCCATC 66
OY 755 TGTACACCTTGGAGAGCGCCGACACCTTCTAGACCTCTGAGACGAGTGAAGATCT 814
Db 67 TGTACACCTTGGAGAGCGCCGACACCTTCTAGACCTCTGAGACGAGTGAAGATCT 126
OY 815 GCACCTGTCAGTTGGTGGTAACAGCTGAGACCCCTGCTACCCGAGACCGAGCGCG 874
Db 127 GCACCTGTCAGTTGGTGGTAACAGCTGAGACCCCTGCTACCCGAGACCGAGCGCG 186
OY 875 TCTGCGCGGAGTGAATGGTGGTGGAGACGAGTGGCCAGAGAGCTTGGCCCGCTG 934
Db 187 TCTG-CGCGANGTGATGATGCTGTGGA-CAGTTGCCAGAGAGA-NCTTGGCCCGCTG 243
OY 935 CTGCGCCGACACTCTGCCAGAGTCCCGAGCGGCTGCGCAGCCA--TGATGCTGACGC 992
Db 244 CTGCGCCGACACTCTGCCAGAGTCCCGAGCGGCTGCGCAGCCAATGANTGCTGACGC 303
OY 993 GGGCGCGAGCTCTAGACGCTG-ATGACCGCGTCCC-AGCGCGCGCTGGAAG 1045
Db 304 GGGCGCGAGCTCTAGACGCTGATGAGCGGCTGCCAAGCGCGCGCTGGAAG 358

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W31516 (TM)

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Distribution rights by Oxford Molecular Ltd

MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 25 22:22:14 2000; Maspar time 13.99 Seconds
724.413 Million cell updates/sec
Tabular output not generated.

Title: >US-09-314-889-2
Description: (1-428) from US09314889.pep
Perfect Score: 3267
Sequence: 1 MEETQCGEARQGRLRGESAA.....ERMGLDCVEDLRSLRQGRP 428

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 35.731; Variance 153.828; scale 0.232

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3267	100.0	428	W31516	Death domain containin	0.00e+00
2	3267	100.0	428	W95537	Death domain containin	0.00e+00
3	3118	95.4	417	W31517	Death domain containin	4.51e-293
4	3118	95.4	417	W26709	Human apoptosis protei	4.51e-293
5	3118	95.4	417	W95538	Death domain containin	4.51e-293
6	3118	95.4	417	W57045	Human apoptosis induci	4.51e-293
7	3118	95.4	833	W64486	Human DR3 protein.	4.51e-293
8	1962	60.1	411	W57046	Mouse apoptosis induci	6.35e-178
9	1342	41.1	181	W26708	Human apoptosis protei	1.40e-116
10	503	15.4	65	W93610	Human DR3 protein frag	4.88e-35
11	412	12.6	909	W64485	Human Fas protein.	1.74e-26
12	408	12.5	455	R07451	Human TNF inhibitor pre	4.12e-26
13	407	12.5	455	R10986	30KD TNF inhibitor pre	5.10e-26
14	407	12.5	455	R75084	p55 TNF-R.	5.10e-26
15	407	12.5	455	R42059	Lambda derived TNF-R.	5.10e-26
16	404	12.4	455	R12082	Human 55KD TNF-binding	9.71e-26
17	404	12.4	455	R20787	TNF-alpha binding prot	2.29e-25
18	400	12.2	443	R51033	Mutant p55 tumour necr	2.29e-25
19	400	12.2	455	R51034	Mutant p55 tumour necr	2.29e-25
20	400	12.2	455	R42197	p55 Tumour necrosis fa	2.29e-25
21	394	12.1	455	R12850	Type I TNF receptor.	8.27e-25
22	387	11.8	433	R51032	Mutant p55 tumour necr	3.69e-24
23	372	11.4	455	R24000	TNF-alpha 55KD recepto	9.05e-23

24	351	10.7	461	R07450	Rat Tumour Necrosis Fa	7.82e-21
25	271	8.3	256	W33357	TBP(20-161)/hCG-alpha f	1.43e-13
26	248	7.6	336	W33560	TBP(20-190)/hCG-beta f	1.58e-11
27	245	7.5	108	W35370	Cytoplasmic domain of	2.91e-11
28	246	7.5	199	R24080	Truncated TNF-alpha 55	2.38e-11
29	246	7.5	211	W89225	Tumour necrosis factor	2.38e-11
30	245	7.5	285	W33359	TBP(20-190)/hCG-alpha f	2.91e-11
31	246	7.5	307	W33358	TBP(20-161)/hCG-beta f	2.38e-11
32	246	7.5	309	R70108	TNF-R-GBPH fusion prot	2.38e-11
33	246	7.5	311	W89229	Tumour necrosis factor	2.38e-11
34	246	7.5	366	W89228	Tumour necrosis factor	2.38e-11
35	246	7.5	371	R07449	Tumour Necrosis Factor	2.38e-11
36	246	7.5	397	W89227	Tumour necrosis factor	2.38e-11
37	246	7.5	417	W89226	Tumour necrosis factor	2.38e-11
38	246	7.5	420	W89224	Tumour necrosis factor	2.38e-11
39	246	7.5	451	R70107	TNF-R-GBP 130 fusion p	2.38e-11
40	246	7.5	547	R70104	TNF-R-GBPH fusion prot	2.38e-11
41	246	7.5	900	R70103	TNF-R-GBP 130 fusion p	2.38e-11
42	246	7.5	1245	R70106	TNF-R-Pl. vivax Duffy	2.38e-11
43	246	7.5	1604	R70105	TNF-R-EBA 175 fusion p	2.38e-11
44	243	7.4	884	R70109	TNF-R-GBP 130 fusion p	4.37e-11
45	240	7.3	161	R27496	Native 30 KD TNF inhib	8.03e-11

ALIGNMENTS

RESULT	ID	Location/Qualifiers
1	W31516	standard; Protein; 428 AA.
AC	W31516;	
DT	02-MAR-1998	(first entry)
DE	Death domain containing receptor DR3-VI.	
KW	Death domain containing receptor; DR3-VI; human; apoptosis;	
OS	Inflammation; NF-kappaB.	
FH	Homo sapiens.	
FT	Key	
FT	Peptide	Location/Qualifiers
FT	1..35	/label=Sig-peptide
FT	36..212	
FT	213..235	/note="extracellular domain"
FT	236..428	/note="transmembrane domain"
FT	353..419	/note="intracellular domain"
FT	1..22	/note="death domain"
FT	33..56	/note="antigenic region (Claim 16)"
FT	59..82	/note="antigenic region (Claim 16)"
FT	95..112	/note="antigenic region (Claim 16)"
FT	122..133	/note="antigenic region (Claim 16)"
FT	161..177	/note="antigenic region (Claim 16)"
FT	179..190	/note="antigenic region (Claim 16)"
FT	196..205	/note="antigenic region (Claim 16)"
FT	196..205	/note="antigenic region (Claim 16)"
PN	W09733904-A1.	
PD	18-SEP-1997.	
PF	17-OCT-1996; U16849.	
PR	12-MAR-1996; US-013285.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(UNMI) UNIV MICHIGAN.	
PI	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;	
DR	WFI, 97-470812/43.	
DR	N-PSDB; T89426.	
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-VI	
PT	for activation of apoptosis and NF-kappaB, antagonists can be used	
PT	to treat inflammatory diseases	

PS Claim 1 Page 71-73: 108pp: English.
CC This protein comprises human death domain containing receptor
CC DR3-V1, a novel member of the tumour necrosis factor receptor
CC family. Its amino acid sequence was deduced from a cDNA clone
CC (see E89426) isolated from a human testis tumour library. Related
CC death domain containing receptor DR3 (see W31517) has also been
CC identified. Recombinant full-length or mature DR3-V1 can be
CC expressed in transformed host cells. These polypeptides can be
CC used to treat diseases and disorders associated with the inhibition
CC of apoptosis, or to screen for modulator compounds. Antagonists,
CC such as antibodies raised against DR3-V1, can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.
SQ Sequence 428 AA;

```
Query Match      100.0%; Score 3267; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	MEETQOGAPRGQJRGESAAVPOALLVLLGARAOGSTRSPDCDAGDFHKKIGLFCGR	60
Qy	1	MEETQOGAPRGQJRGESAAVPOALLVLLGARAOGSTRSPDCDAGDFHKKIGLFCGR	60
Db	61	GCSPAGHYLKADCTEPGCGNSTCLVCRODTFLAMENHNHNSCARCOACDQASQVAALENCSA	120
Qy	61	GCSPAGHYLKADCTEPGCGNSTCLVCRODTFLAMENHNHNSCARCOACDQASQVAALENCSA	120
Db	121	VADPRCGCKPEWFMFECQVSOQVSSPPYCOPLDCGALLHHHTRLTLCRRPTDGTCLPGF	180
Qy	121	VADPRCGCKPEWFMFECQVSOQVSSPPYCOPLDCGALLHHHTRLTLCRRPTDGTCLPGF	180
Db	181	YEHGDCVCSCTSTLGSCEPCECAVCCGWRQMFVQVLLAGLVNPLLGATLLYTYRRCHWP	240
Qy	181	YEHGDCVCSCTSTLGSCEPCECAVCCGWRQMFVQVLLAGLVNPLLGATLLYTYRRCHWP	240
Db	241	HKPLVTTADAEAGMEALTPPPATHLSPIDSAHTLLAPRPSSEKICTVQVVGSMWPGVPEQO	300
Qy	241	HKPLVTTADAEAGMEALTPPPATHLSPIDSAHTLLAPRPSSEKICTVQVVGSMWPGVPEQO	300
Db	301	BALCPQVWVMSMDQJLPSRALGPAAAPTLSPESPAGSPAMMLQPGQVLYDVMDVAVPARMKKE	360
Qy	301	BALCPQVWVMSMDQJLPSRALGPAAAPTLSPESPAGSPAMMLQPGQVLYDVMDVAVPARMKKE	360
Db	361	FVVRTIGLBEAELEAVEVEIGFRRODOQIBMLKRMKQOOPAGIGAYTAAALERMGLDGCYEDL	420
Qy	361	FVVRTIGLBEAELEAVEVEIGFRRODOQIBMLKRMKQOOPAGIGAYTAAALERMGLDGCYEDL	420
Db	421	RSRLORGP	428
Qy	421	RSRLORGP	428

RESULT	2	
ID	W95537	standard; Protein; 428 AA.
AC	W95537.	
DT	25-MAR-1999	(first entry)
DE	Death domain containing receptor polypeptide (DR3-V1)	
KW	Death domain; receptor; DR3-V1; DR3; recombinant.	
OS	Homo sapiens.	
PH	Key	
FT	Peptide	Location/Qualifiers
FT		1..35
FT	Protein	/note="signal peptide"
FT		36..428
FT		/note="mature protein"
PN	J11000170-A.	
PD	06-JAN-1999.	
PF	12-MAR-1997.	057503.
PR	06-FEB-1997.	US-037341.
PR	12-MAR-1996.	US-013285.
PR	17-OCT-1996.	US-028711.
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(UNMT) UNIV MICHIGAN.	
DR	WPI: 99-124390/11.	

DR N-PSDB; X00924.
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 1; Fig 1, 2; 50pp; Japanese.
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are used
CC for the recombinant production of the proteins. The present sequence
CC represents the amino acid sequence of a death domain containing receptor
CC polypeptide (DR3-VI).
SQ Sequence 428 AA;

Query Match	100.0%;	Score 3267;	DB 1;	Length 428;
Best Local Similarity	100.0%;	Pred. No. 0.00e+00;		
Matches 428; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Db	1	MEMDOOGAPRGOLRGESAAVPOALLLVLLGARAOGSTRSPRODCAGDPHKKIGLFCR	60
Oy	1	MEETIOGGAAPRGOLRGESAAVPOALLLVLLGARAOGSTRSPRODCAGDPHKKIGLFCR	60
Db	61	GCPSAHTYKACBTEPCGNSCTLCVCPDPTFLAMENHNHNSCARQACDEQASOVALENCSSA	120
Oy	61	GCPSAHTYKACBTEPCGNSCTLCVCPDPTFLAMENHNHNSCARQACDEQASOVALENCSSA	120
Db	121	VADPTGCGKPRMFEVCOYSSQCVSSSPFYCCPCLDCCGLNHTRTLCSRRPTDGTCLPRG	180
Oy	121	VADPTGCGKPRMFEVCOYSSQCVSSSPFYCCPCLDCCGLNHTRTLCSRRPTDGTCLPRG	180
Db	181	YEHGDCVSCPTSTLSCSPERCAAVCGMROMFWVOYLLAGLVVPLLGAFTLYTTRHCP	240
Oy	181	YEHGDCVSCPTSTLSCSPERCAAVCGMROMFWVOYLLAGLVVPLLGAFTLYTTRHCP	240
Db	241	HRPLTADACMEALTPRPATNLSPLDSANTLLARPDSSEKTCYVOLVGNSSMTGRPETO	300
Oy	241	HRPLTADACMEALTPRPATNLSPLDSANTLLARPDSSEKTCYVOLVGNSSMTGRPETO	300
Db	301	EALCPOVTWMSMDOLPFSRALGPAAPTLSPESPAGSPAMMIQOPGOLYDVADAVPARMK	360
Oy	301	EALCPOVTWMSMDOLPFSRALGPAAPTLSPESPAGSPAMMIQOPGOLYDVADAVPARMK	360
Db	361	FVRTLGLBAETEAVEVEIGFRPOOQIEMLKRMQOORPAGIYAAALEMGLDGCYEDL	420
Oy	361	FVRTLGLBAETEAVEVEIGFRPOOQIEMLKRMQOORPAGIYAAALEMGLDGCYEDL	420
Db	421	RSRLORGP 428	
Oy	421	RSRLORGP 428	

RESULT	3
ID	W31517 standard; Protein; 417 AA.
AC	W31517;
DT	02-MAR-1998 (first entry)
DE	Death domain containing receptor DR3.
KE	Death domain containing receptor; DR3-V1; human; apoptosis;
KW	inflammation; NF-kappaB.
OS	Homo sapiens.
FH	Key
FT	Peptide
FT	1..24
FT	/Label= Sig_peptide
FT	25-201
FT	/note= "extracellular domain"
FT	202..224
FT	/note= "transmembrane domain"
FT	225..417
FT	/note= "intracellular domain"
FT	342..408
FT	/note= "death domain"
FT	
FT	
PN	W09733904-A1.
PD	18-SEP-1997
PF	17-OCT-1996; UI6849.

PR 12-MAR-1996; US-013285.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PI Dillon PJ Dixit VM, Gentz RL, Ni J, Yu G;
DR WPI: 97-470812/43.
DR N-PSDB: T89427.
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
PS Claim 1; Page 75-77; 108pp; English.
CC This protein comprises human death domain containing receptor
CC DR3, a novel member of the tumour necrosis factor receptor
CC family. Its amino acid sequence was deduced from a cDNA clone
CC (see T89427) isolated from a HUVEC cDNA library. Related death
CC domain containing receptor DR3-V1 (see W31516) has also been
CC identified. Recombinant full-length or mature DR3, or the
CC extracellular, transmembrane, intracellular or death domain of
CC DR3 can be expressed in transformed host cells. These polypeptides
CC can be used to treat diseases and disorders associated with the
CC inhibition of apoptosis, or to screen for modulator compounds.
CC Antagonists, such as antibodies raised against DR3-V1, can be used
CC to treat diseases and disorders associated with increased apoptosis
CC and for treating inflammatory diseases and disorders.
SQ Sequence 417 AA;

Query Match 95.4%; Score 3118; DB 1; Length 417;
Best Local Similarity 98.3%; Pred. No. 4,51e-293;
Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 4 RPRGCAVAALALLVLLGARAAGGTRSPRCDAGDFHKITGLFCCRCGPAHYLKAPCTE 63
QY 15 RGSAAVPVQALLVLLGARAAGGTRSPRCDAGDFHKITGLFCCRCGPAHYLKAPCTE 74
Db 64 PCGNSTCLVCPQDTFLAMENHNHNSCARQACDEQASQVALENCSSAVALTRCGCKPGWFEV 123
QY 75 PCGNSTCLVCPQDTFLAMENHNHNSCARQACDEQASQVALENCSSAVALTRCGCKPGWFEV 134
Db 124 ECVQSCVSSSPFYCOPCLDCGALHRTLRILCSRRDTCGTLPGFYEHDGCVSCPST 183
QY 135 ECVQSCVSSSPFYCOPCLDCGALHRTLRILCSRRDTCGTLPGFYEHDGCVSCPST 194
Db 184 LGSCPERCAAVCGMRQMFVQVLLAGLVPLLGATLTYTYRHCPHKLVTADAEAGMEA 243
QY 195 LGSCPERCAAVCGMRQMFVQVLLAGLVPLLGATLTYTYRHCPHKLVTADAEAGMEA 254
Db 244 LTPPATLHSLPDSAHNTLLAPDSSSEKICTVOLVGNSTWTPGYPETOALCPQVWMSMDOL 303
QY 255 LTPPATLHSLPDSAHNTLLAPDSSSEKICTVOLVGNSTWTPGYPETOALCPQVWMSMDOL 314
Db 304 PSRALGPAAAPTLSPESPAGSPAMMLQPGPOLVDVMDAVPARRKKEFVRTLGLREAEIEA 363
QY 315 PSRALGPAAAPTLSPESPAGSPAMMLQPGPOLVDVMDAVPARRKKEFVRTLGLREAEIEA 374
Db 364 VEVEIGRFDOQYEMLKRWRQOQAGIGAVYAALERMGLDGCVEEDLSRLQGRP 417
QY 375 VEVEIGRFDOQYEMLKRWRQOQAGIGAVYAALERMGLDGCVEEDLSRLQGRP 428

RESULT 4
ID W26709 standard; Protein; 417 AA.
AC W26709;
DT 14-APR-1998 (first entry)
DE Human apoptosis protein Apo-3.
KW Apo-3; apoptosis; human; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= Sig-peptide
FT Domain 25..198
FT /note= "extracellular domain"
FT Domain 199..224
FT /note= "transmembrane domain"
FT Domain 225..417

FT FT /note= "intracellular domain"
FT Domain 338..417
FT /note= "death domain"
FT Modified_site 67
FT /note= "N-glycosylated"
FT Modified_site 106
FT /note= "N-glycosylated"
PN W09737020-A1.
PD 09-OCT-1997.
PF 31-MAR-1997; U05230.
PR 23-SEP-1996; US-710802.
PR 01-APR-1996; US-625328.
PA (GETH) GENENTECH INC.
PI Ashkenazi AJ;
DR WPI: 97-503105/46.
DR N-PSDB: T91180.
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
PS Claim 19; Page 46-48; 70pp; English.
CC This novel polypeptide, designated Apo-3, is a protein that
CC stimulates or induces apoptotic activity in mammalian cells
CC purposes. Its amino acid sequence was deduced from a human foetal
CC heart cDNA clone (see T91180). The N-terminal 181 amino acids of
CC Apo-3 are identical to the sequence of another novel apoptosis
CC polypeptide, Apo-2LI (see W26709). Also claimed are: polypeptides
CC comprising the extracellular or death domain of Apo-3; chimeric
CC molecules comprising Apo-3 fused to a heterologous amino acid
CC sequence; antibodies that bind to Apo-3 or its extracellular
CC domain; nucleic acids encoding the polypeptides, as well as
CC vectors and host cells; a non-human transgenic animal containing
CC cells that express nucleic acid encoding Apo-3; and a non-human
CC knockout animal containing cells having an altered Apo-3 gene.
CC Apo-3 can be used to induce apoptosis or NF-kappa-B- (NF-kB) - or
CC JNK-mediated gene expression for therapeutic purposes. Apo-3-19G
CC fusion proteins can be used to inhibit apoptosis or NF-kB
CC induction or JNK activation for therapeutic purposes, and can
CC be used as immunogens for anti-Apo-3- antibody production.
CC Apo-3 or Apo-2LI can also be used as assay standards. The
CC animals can be used in drug screening and development.
SQ Sequence 417 AA;

Query Match 95.4%; Score 3118; DB 1; Length 417;
Best Local Similarity 98.3%; Pred. No. 4,51e-293;
Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 4 RPRGCAVAALALLVLLGARAAGGTRSPRCDAGDFHKITGLFCCRCGPAHYLKAPCTE 63
QY 15 RGSAAVPVQALLVLLGARAAGGTRSPRCDAGDFHKITGLFCCRCGPAHYLKAPCTE 74
Db 64 PCGNSTCLVCPQDTFLAMENHNHNSCARQACDEQASQVALENCSSAVALTRCGCKPGWFEV 123
QY 75 PCGNSTCLVCPQDTFLAMENHNHNSCARQACDEQASQVALENCSSAVALTRCGCKPGWFEV 134
Db 124 ECVQSCVSSSPFYCOPCLDCGALHRTLRILCSRRDTCGTLPGFYEHDGCVSCPST 183
QY 135 ECVQSCVSSSPFYCOPCLDCGALHRTLRILCSRRDTCGTLPGFYEHDGCVSCPST 194
Db 184 LGSCPERCAAVCGMRQMFVQVLLAGLVPLLGATLTYTYRHCPHKLVTADAEAGMEA 243
QY 195 LGSCPERCAAVCGMRQMFVQVLLAGLVPLLGATLTYTYRHCPHKLVTADAEAGMEA 254
Db 244 LTPPATLHSLPDSAHNTLLAPDSSSEKICTVOLVGNSTWTPGYPETOALCPQVWMSMDOL 303
QY 255 LTPPATLHSLPDSAHNTLLAPDSSSEKICTVOLVGNSTWTPGYPETOALCPQVWMSMDOL 314
Db 304 PSRALGPAAAPTLSPESPAGSPAMMLQPGPOLVDVMDAVPARRKKEFVRTLGLREAEIEA 363
QY 315 PSRALGPAAAPTLSPESPAGSPAMMLQPGPOLVDVMDAVPARRKKEFVRTLGLREAEIEA 374
Db 364 VEVEIGRFDOQYEMLKRWRQOQAGIGAVYAALERMGLDGCVEEDLSRLQGRP 417
QY 375 VEVEIGRFDOQYEMLKRWRQOQAGIGAVYAALERMGLDGCVEEDLSRLQGRP 428

DB	375	RLGSDHEIDRLDELONGCLREAOYSLMAYTRRRPRREATLLELGRVLRMDLGGLED	434
OY	364	TLGLEAELEAVEVEIGR-FRDOOYEMLRKRRDOP--AGLGAVALLERMGJGDGVED	419
DB	435	IEEAL 439	
OY	420	LR SRL 424	
RESULT 12			
ID	R07451	standard: protein; 455 AA.	
AC	R07451:		
DT	29-JAN-1991	(first entry)	
DE	Human Tumour Necrosis Factor- α -Receptor from lambdaTNF-R2 cDNA insert.		
KW	Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;		
KW	infectious disease; parasitic disease; cachexia;		
KW	autoimmune disease; shock; lambdaTNF-R2; ratNF-R8.		
OS	Homo sapiens.		
PN	EP-393438-A.		
PD	24-OCT-1980.		
PF	06-APR-1990; 106624.		
PR	21-APR-1989; DE-913101.		
PR	21-JUN-1989; DE-920282.		
PA	(BOEH) BOEHRINGER INGELHEIMINT.		
PI	Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;		
DR	Wp1: 90-321987/43.		
DR	N-PSDB: 006285.		
PT	DNA encoding TNF binding protein and TNF-receptor - action in		
PT	tumour treatment and to understand mechanisms to TNF action		
PS	Disclousure: Fig 91(1-2): 51pp: German.		
CC	ratNF-R8 (006284) was used to screen the HS913T cDNA library.		
CC	lambdaTNF-R2 encodes the complete human TNF-R2 and was used to		
CC	construct a plasmid (pADTNF-R) expressing the product the same way		
CC	as pADTNF-BP (see 006282). The expressed proteins are useful		
CC	biochemically and therapeutically to control disorders which		
CC	involve the damaging effects of TNF-alpha or -beta (e.g. infectious or		
CC	parasitic diseases, shock, cachexia, autoimmune diseases, adult		
CC	respiratory distress syndrome etc., or side effects of treatment with		
CC	TNF-alpha). They can also be used as diagnostic reagents for		
CC	assaying TNF and in study of TNF-receptor interactions.		
CC	See also 006282-006285.		
CC	Sequence 455 AA;		
Query Match	12.5%;	Score 408;	DB 1; Length 455;
Best Local Similarity	29.9%;	Pred. No. 4,12e-26;	
Matches 127;	Conservative 81;	Mismatches 177;	Indels 40; Gaps 32.
DB	27	VIGLPHLGDEKEDKDSVCPQGYTHPNONNSICCTCKHKGTYLYNDGPGQDTPDCRECS	86
OY	30	LLGARAGQGTSPR-CDDA-GDF-HKKIGLFCGCGCAGHILKAPCEPCGNSTGLYCPQ	86
DB	87	GSFLASSENHLR-HCLSCSKCKREKGOVEISSCTVDRTPTVCGCKRKNQRYHW-SENIFQC-	143
OY	87	DTFLAMENHNHNSDCARQACDEQASQVALENCSSVAADTRCGCKRGWVEQVSQVSSSP	146
DB	144	ENCSLECN-GTVH----LSCQKQNTVC-CHAGFPLRENDVSCSKSKSLBCTKTLCLP	197
OY	147	FYCPQCLDCGALHNRHLIC-SKRDTCGCTLPGFETHGDCVSCSPSTLG-SCPEHC-A	203
DB	198	QIQNVKCTEDSGTIVLLP-LVIFPGCLLSLPLTGLMYRYQRMKSLYSIVCGSKSPKE	256
OY	204	AVCGMRQMF-W-VQVLLAGLVV--PL-LLGATIL-YTYR-HCPWHK--PLTVADEA-GME	253
DB	257	GELGGTTTKPLAPNPSTSPPTGFTPTLGLFSVPSSTTSSSTYTPGCGCPNFAARREYAP	316
OY	254	A-LTPPRATHSLPDS-AHTL-LAPPDSEKICIVQVLGNS-WTPGVPEYQALCPQYT-	308
DB	317	PYQAGADPLIALTASDPILPNPLQKEDSARHPQSLDTPDATIYAAYENPPLRMKFEVR	376
OY	309	-W-SMDLPRBALCPAAPT-LSP-ESPAGSPAMMLDQPGQ-LYDVADVAPARRMKFEVR	363
DB	377	RLGSDHEIDRLDELONGRCLEAOYSMLATWRRRTPRREATLLELGRVLRMDLGGLED	436

[illegible]

QY 420 LRSRL 424

RESULT 14
 ID R75084 standard; Protein; 455 AA.
 AC R75084;
 DT 19-JAN-1996 (first entry)
 DE p55 TNF-R.
 KM p55: tumour necrosis factor receptor; TNF-R; human; murine; chimera;
 KM epidermal growth factor receptor; EGF-R; protease; inhibitor;
 KM phorbol myristate acetate; PMA.
 OS Homo sapiens.
 FH Key
 FT peptide Location/Qualifiers
 FT 41..53
 FT /note= "N terminus of soluble p55 TNF-R"
 FT modified_site 54..56
 FT /note= "glycosylation site"
 FT modified_site 145..147
 FT /note= "glycosylation site"
 FT modified_site 161..163
 FT /note= "glycosylation site"
 FT peptide 193..210
 FT /note= "peptide used in creation of chimeras"
 FT region 198..210
 FT /note= "spacer region"
 FT misc_difference 201
 FT /note= "major C terminus for soluble p55 TNF-R"
 FT misc_difference 202
 FT /note= "essential for shedding reaction"
 FT misc_difference 203
 FT /note= "minor C terminus for soluble p55 TNF-R"
 FT region 212..234
 FT /note= "transmembrane region"
 PN AU9475742-A.
 PD 04-MAR-1993.
 PD 11-OCT-1994; 075742.
 PR 12-OCT-1993; IL-107268.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Balin M, Brakebusch C, Varfolomeev E, Wallach D;
 DR MPI: 95-194342/26.
 DR N-PSDB: Q90513.
 PT New protease capable of cleaving soluble tumour necrosis factor
 PT (TNF) receptor - from cell-bound TNF-receptor, useful for
 PT antagonising deleterious effects of TNF.
 PS Disclosure: Fig 1; 40pp; English.
 CC This sequence represents human p55 tumour necrosis factor (TNF-R).
 CC Expression of this receptor is regulated by shedding of the extracellular
 CC receptor fragment. The p55 TNF-R can be shed in response to different
 CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
 CC type. The only region of the receptor whose structure affects the
 CC shedding response is the spacer region (see R75012) in the extracellular
 CC domain. This region is located close to a site of cleavage of the
 CC molecule, and links the cys rich module to the transmembrane domain. The
 CC spacer region of the encoded protein was used to create the chimeras
 CC between human p55 TNF-R and murine epidermal growth factor receptor
 CC (EGF-R) that are represented by R75007-11. This spacer region was
 CC subjected to deletion mutations (R75013-25) and substitutions
 CC (R75026-47). Of the spacer region, the most important residues are
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
 CC important of these. The shedding of the receptor is independent of the
 CC side chain identity of these residues, with the exception of a limited
 CC dependence on the identity of Val 173. Mutations which alter the
 CC conformation of the protein adversely effect the shedding process.
 CC The mutations shown in R75013-47 were introduced in order to create an
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
 CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
 CC be used for enhancing TNF function.
 SO Sequence 455 AA;

Query Match 12.5%; Score 407; DB 1; Length 455;
 Best Local Similarity 29.9%; Pred. No. 5; 10e-26;
 Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDYSVCPQGGKIHPONNSICQTKCHKGTLYLNDPCPGPDQDRCES 86
 QY 30 LIGARAQGGTSPR-CDDA-GDF-HKKIGLFCRCRCPAGHYLKACPTPCGSGTLCVCPQ 86
 Db 87 GSFTASENHLR-HCISGSKCRKEMQVEISCTYDRTDVTCCGCKKQYHHY-SEMLPQC- 143
 QY 87 DTFLAMENHNHNSCARCACCDEOASOVALRNCASAVADRCCCKPKPMFVECOVSQCVSSSP 146
 Db 144 FNGSLCLN-GTVH---LSCQEKONTVC-TCNAGFELRENECVSCSNCKSIQCTKLCIP 197
 QY 147 FYCQPCDCCGADHRHRLIC-SRRDTCGTCLPGYEHGDCVSCPSTSLG-SCBERC-A 203
 Db 198 QIENYKGTEDSGTWTLP-LVYIFPCLLSLFTGLMRYORMKSLYSIQGKSTPEKE 256
 QY 204 AVCGWRQWF-W-VQYLLAGIYV--PL-LLGATLT-YTYR-HCMPRK--PLTYADBA-GME 253
 Db 257 GELSGTTKPLAPNPSPTPEFTTLGFSPPSSTFTSSSTYTTGGDCPNFAPRREYAP 316
 QY 254 A-LTPPPATHLSPIDS-AHTL-LAPDSSEKICTYQLVGN-S-WTGGYPTQALCPQYT- 308
 Db 317 PYGADPILATALASDPINPLQKWECSAHKPOSIDTDDPATLYAVENVPEPLRKKEFVR 376
 QY 309 -W-SWDQLPSRLGPAAPF-LSP-ESPAQSPAMMLQFQPO-LYVMDAVPARMKKEFVR 363
 Db 377 RLGLSDHEIDRLLELQNGRLREAOYSMLATWRRRTPRRATLELLGRVLRMDLLGCTLED 436
 QY 364 TLGLREAELEAVEVEIGR-FRDQYEMLRKMRQOP---AGLGAVYALERMGIDGCVED 419
 Db 437 IEEL 441
 QY 420 LRSRL 424

RESULT 15
 ID R42059 standard; Protein; 455 AA.
 AC R42059;
 DT 29-APR-1994 (first entry)
 DE Lambda derived TNF-R.
 KM Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 KM IL-1R; fusion protein; linker: TNF; IL-1; cachexia; cerebral malaria;
 KM rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
 KM pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 KM graft versus host disease; sepsis; inflammation; allergy;
 KM autoimmune dysfunction.
 OS Homo sapiens.
 OS Lambda-glt10-7ctnfbp.
 FH Key
 FT peptide Location/Qualifiers
 FT 1..40
 FT /note= "Signal peptide"
 FT protein 41..455
 FT /note= "Mature hTNF-R"
 PN M09319777-A.
 PD 14-OCT-1993.
 PD 26-MAR-1993; U02938.
 PR 30-MAR-1992; US-860710.
 PA (IMV) IMMUNEX CORP.
 PI Smith CA;
 DR MPI: 93-336592/42.
 DR N-PSDB: Q49932.
 PT New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 PS Disclosure: Page 57-59; 85pp; English.
 CC The sequences given in R42058-59 represent human tumour necrosis
 CC factor receptor (TNF-R) and the sequences in R42060-61 represent
 CC human interleukin-1 receptor (IL-1R). These sequences were used in
 CC the production of a fusion protein which conformed to one of the
 CC formulae:
 CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 25 22:21:31 2000; MasPar time 23.74 Seconds
 Tabular output not generated. 850.475 Million cell updates/sec

Title: >US-09-314-889-2
 Description: (1-428) from US09314889.pep
 Sequence: 1 MEPTQGEAPRGQLRGESAA.....ERMGLDGCVEDLRSLRQGP 428

Scoring table: PAM 150
 GAP 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r64
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 47.837; Variance 92.768; scale 0.516

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	407	12.5	455	1	GOHUT1	tumor necrosis factor
2	399	12.2	454	1	GOMST1	tumor necrosis factor
3	388	12.2	461	2	JC4302	tumor necrosis factor
4	385	11.8	454	2	I57826	tumor necrosis factor
5	383	11.7	461	1	GOMST1	tumor necrosis factor
6	211	6.5	324	2	JC2395	Fas antigen precursor
7	204	6.2	327	2	A46484	apoptosis mediating m
8	190	5.8	314	2	I37383	Fas soluble protein -
9	180	5.8	335	2	A40036	apoptosis mediating s
10	182	5.6	326	1	GOVZML	T2 protein - myxoma v
11	179	5.5	349	2	D36858	gene G4R protein - va
12	177	5.4	260	1	A46517	CD27 antigen precursor
13	165	5.1	271	2	S12783	OX40 antigen precursor
14	167	5.1	272	2	I48700	gene OX40 protein - m
15	168	5.1	461	1	A35356	tumor necrosis factor
16	164	5.0	325	2	B43692	T2 protein - rabbit f
17	159	4.9	277	2	A60771	B-cell activation pro
18	160	4.9	435	2	I54182	tumor necrosis factor
19	161	4.9	474	2	B38634	tumor necrosis factor
20	158	4.8	250	1	A49053	CD27 antigen precursor
21	157	4.8	459	1	I48854	gene murine tumour ne
22	153	4.7	656	2	I49299	receptor interacting
23	146	4.5	416	1	JN0006	nerve growth factor r

24	139	4.3	427	1	GOHUN	nerve growth factor r
25	134	4.1	372	2	I38992	receptor interacting
26	134	4.1	671	2	T09479	serine/threonine prot
27	131	4.0	425	1	A26431	nerve growth factor r
28	125	3.8	132	2	S57662	Fas/Apo-1/CD95 protei
29	125	3.8	149	2	S58666	Fas-Delta-(4,7) prote
30	124	3.8	1808	2	T15099	hypothetical protein
31	124	3.8	3635	2	T10053	laminin alpha 5 chain
32	121	3.7	1574	2	T13954	MEGF6 protein - rat
33	117	3.6	407	2	C70816	hypothetical protein
34	116	3.6	799	2	A38308	integrin beta-5 chain
35	114	3.5	277	2	I37552	OX40 homology - human
36	114	3.5	1247	1	MMHUND	nidogen precursor - h
37	110	3.4	289	2	A46515	B cell-associated sur
38	110	3.4	305	2	A46476	CD40 - mouse
39	111	3.4	656	2	JC2005	integrin beta-5 chain
40	111	3.4	1607	1	MMHUB2	laminin gamma-1 chain
41	112	3.4	1609	1	MMHUB2	laminin gamma-1 chain
42	108	3.3	103	2	A42523	A53R protein - vaccin
43	109	3.3	571	2	C75165	glutanyl-tRNA synthet
44	109	3.3	1790	1	MMFEB1	laminin beta-1 chain
45	109	3.3	3707	2	S18252	heparan sulfate prote

ALIGNMENTS

RESULT ENTRY	1	ALIGNMENTS
GOHUT1	#type complete	
tumor necrosis factor precursor	- human	
P55 tumor necrosis factor receptor: TNF receptor		
tumor necrosis factor alpha inhibitor: tumor necrosis factor		
binding protein 1 (TNF blocking factor)		
ORGANISM	#formal_name Homo sapiens #common_name man	
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999	
ACCESSIONS	A38208; A34899; A34900; A36555; C36555; A38281; S12057; J07058; A60231; A38258; A60594; A35010; JC2404	
REFERENCE	A38208	
#authors	Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.	
#journal	Genomics (1992) 13:219-224	
#title	Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to chromosome 12p13.	
#cross-references	MUID:92250049	
#accession	A38208	
##molecule_type	DNA	
##residues	1-455	
##cross-references	GB:M75864; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g339750	
REFERENCE	A34899	
#authors	Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.	
#journal	Cell (1990) 61:351-359	
#title	Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.	
#cross-references	MUID:90235284	
#accession	A34899	
##molecule_type	mRNA	
##residues	1-455	
##cross-references	GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754	
##experimental_source	part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing	
##note		
REFERENCE	A34900	
#authors	Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.	
#journal	Cell (1990) 61:361-370	
#title	Molecular cloning and expression of a receptor for human tumor necrosis factor.	
#cross-references	MUID:90235285	
#accession	A34900	
##molecule_type	mRNA	

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##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
REFERENCE
#authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
# Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
# Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
#accession C36555
##molecule_type protein
#title 30-38:41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'X', 100-104;
107-128:162-167, 'X', 169-201 ##label HIZ
#residues the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor
#note
REFERENCE
#authors A38281
Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
#note The authors translated the codon TGG for residue 371 as
Thr, AAG for residue 372 as Leu, and GAC for residue
427 as Asn
REFERENCE
#authors S12057
Nophr, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
R.; Adert, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-RS).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:9106021
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NGP
##cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing
REFERENCE
#authors JT0758
Kemper, O.; Wallach, D.
#journal Gene (1993) 134:209-216
#title Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#cross-references MUID:94085779
#accession JT0758
##molecule_type DNA
##residues 1-13 ##label KEM
REFERENCE
#authors A60231
Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
#residues 41-43, 'X', 45-53, 'X', 55-57 ##label SEC
REFERENCE
A38258

```

```

#authors Gatana, T.; Hwang, C.; Kohn, W.; Cappuccini, F.; Lucchi III,
R.A.; Jeffes, E.W.B.; Lentz, R.; Tomlich, J.; Yamamoto,
J.S.; Granger, G.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title Purification and characterization of an inhibitor (soluble
tumor necrosis factor receptor) for tumor necrosis factor
and lymphotoxin obtained from the serum ultrafiltrates of
human cancer patients.
#cross-references MUID:91062364
#accession A38258
##molecule_type protein
#residues 41-60 ##label GAT
##experimental_source cancer patient serum
REFERENCE
#authors A60594
Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
Grubb, A.; Adolf, G.
#journal Eur. J. Haematol. (1989) 42:270-275
#title Isolation and characterization of a tumor necrosis factor
binding protein from urine.
#cross-references MUID:89171156
#accession A60594
##molecule_type protein
#residues 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 ##label OLS
##experimental_source renal failure patient urine
REFERENCE
#authors A35010
Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
##molecule_type protein
#residues 41-45 ##label ENG
##experimental_source normal urine
REFERENCE
#authors JC2404
Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#cross-references MUID:95128033
#accession JC2404
##molecule_type protein
#residues 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201
##label KAJ
##experimental_source urine
COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).
GENETICS
#gene GDB:TNFR1
#cross-references GDB:125913; OMIM:191190
#map_position 12p13.2-12p13.2
#introns 13/3: 65/71; 106/71; 158/72; 209/71; 247/71; 256/73; 353/71
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-21
22-455
30-211
41-201
44-82
84-126
127-167
168-196
212-234
235-455
54,145,151
SUMMARY
#length 455 #molecular_weight 50494 #checksum 153

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Query Match	Similarity	Score	DB 1:	Length
27	VGLVPLHLDRKRDVCPQKGIHPONNNSICTCKHKGYLVNDPCGPDDTCRCES	12.5%	DB 1:	455
30	LLGARAQGTSPR-CDCA-GDF-HKKIGLFCRCRGRAGHYLAPRCPGNSTCLVCPQ	29.9%	DB 1:	479e-55
87	GSFTASENHLR-HCLSCSKCKREMGVEISSCTVDRTVCGCRNDYRHYW-SENLFQC	81:	Mismatches 177:	Gaps 32:
87	DFFLAWENHNHSEACRQACDEQASQVALENCASAVADTRCGCKPGMFEVQVSCVSSP			
144	FNCISCLN-GYH----LSCQEKQNTVC-TCHAGFLPREECYSCSKSKSLCTKCLCP			
147	FYCOPCLDGAHLHRTLLC-SRRDDCGCLGFEYHEDGCVSCPSTIG-SCPERC-A			
198	OYENYKGTEDSGTYLLP-LVTFEGCLSLLEIGLRYFRQMKSKYSTIVCGSTPEKE			
204	AVCGMRQW-W-VQVLLAGLV-PL-LIGATLT-YTYR-HCMPHK-PLVYTADEA-GME			
257	GELEGTTRKPLAPNPSFSPGFTPLPLGSPVBSSTFTSSSTYKPGDCPNFAARRVAP			
254	A-LTPRPATHLSPDS-AHTL-LAPDSSSEKICTVQVGN-SWPGVPEQALCPQT			
317	PVQAGDPILATLALASPIPLNPLQKWDSSAHKPOSLOTDPATLYAVENPPLRKFEVR			
309	-W-SMDQLPSRALGPAAPLT-LSP-ESPAGSPAMMLQPGQ-LYVDADAVPARMKFEVR			
377	RGLSDHEIDRLRLOGLRCLREAOYSMLTWRRRTPRRATLELLGVLNDMDLGLCLED			
364	TGLLEAELEAVEYEIGR-FRDOQYELMKRROOP---AGLQAVYALALRMGLGCEVD			
437	IEEAL 441			
420	LSRSL 424			

	p53 tumor necrosis factor receptor.
#cross-references MUID:91285014	
#accession S16677	
##molecule_type mRNA	
##residues 1-454 ##label BAR	
REFERENCE S19021	
##authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.	
##journal Immunogenetics (1991) 34:338-340	
##title Molecular cloning and expression of the mouse Tnf receptor type b.	
#cross-references MUID:92039815	
#accession S19021	
##molecule_type mRNA	
##residues 1-454 ##label ROT	
REFERENCE S15432	
##authors Bebo, B.F.	
##journal Immunogenetics (1994) 39:450-451	
##title Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.	
#cross-references MUID:94245292	
#accession I54532	
##status translated from GB/EMBL/DBJ	
##molecule_type mRNA	
##residues 1-454 ##label RES	
##cross-references GIB:D6349; NID:9430732; PIDN:AAA59361.1; PID:94307333	
COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).	
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology	
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein	
FEATURE	
1-29	#domain signal sequence #status predicted #label SIG\
30-454	#product tumor necrosis factor receptor type 1 #status predicted #label MAT\
30-212	#domain extracellular #status predicted #label EXT\
40-82	#domain NGF receptor repeat homology #label NG1\
84-136	#domain NGF receptor repeat homology #label NG2\
127-167	#domain NGF receptor repeat homology #label NG3\
168-204	#domain NGF receptor repeat homology #label NG4\
213-235	#domain transmembrane #status predicted #label MEM\
236-454	#domain intracellular #status predicted #label INT\
54,151,202	#binding-site carboxylate (Asn) (covalent) #status predicted
SUMMARY	#length 454 #molecular-weight 50129 #checksum 4839
Query Match	12.2%; Score 399; DB 1; Length 454;
Best Local Similarity	28.7%; Pred. No. 1,86e-53;
Matches 119; Conservative	79; Mismatches 182; Indels 34; Gaps 28;
Df	40 RDSICLP-OGKVVHKNNSICTCKHKGYLVSDPSRGRTVCRECKGTFTASQNTLR-97
Oy	40 RSPRCDAGDP-HKKIGLFCRCGRPAHGTYLKAPCTECGSGTCLVCYODPDTLAEMNHNS-98
Df	98 QCLSKTCRKMSQVEISPCOADKYOGCKENGFORYLTSETHFOCDSCPFENGVTIP-157
Oy	99 ECARQACDEBSQVALENCASAVADTRCGCKPGMFVCC--QVS-QCYSSSP-FYCOPCLD-154
Df	158 CKETQ-NTVCNCHAGFFLRESECVPC--SHCKNKEDCMKLCLPPPLANTNTNPDSGTAVL-214
Oy	155 CGALHRHRLLC-SR---RDIDCGTCLPGFYEHGDGVCS-CPTSLGSC--PERCAAVCG-207
Df	215 LPIVLILGLCLLSIFITISLMCRYRMRYVSYIICRPVP-VAEERAKG-KPLTPASPAPF-272
Oy	208 WKQMWOVO-LLAGIVPELL-LGATTL-TYYTRH-CWNRKPLVTADEAGMFLPPPATIH-263
Df	273 SPSTGFNFNTLGFSTPGFSSPVSP-ISPJFGSPSNMHFMFPVSEVNYTOGADPLYESLC-331
Oy	264 SPLDS-AHTL-LARPDSSEKICTYQLVGNSMTREYPETGOALCPQV-TWSMDLPKRALG-320
Df	332 SVPAETSVQKKWEDSAHPDRPDNDLATILYAVIDGVPRARKKEFRMGESHEIERLENO-391

QY 321 PAAAPTLSPSPAGS-PAMMLOPG-POLYDVMDAVPARMKKEFVRTIGLREAEIEAVEVE 378

Db 392 NGRCLEAOYSMLAEWRRRTPRHEDTLEVVGLVSKMNLAGEIENTLEAL-RNP 444

QY 379 IGR-FRDOQYEMLKRWRQOP--AG-LGAVYALALERMGLDGCVEDLRSRLQRP 428

RESULT 3

ENTRY JC4302 #type complete

TITLE tumor necrosis factor receptor p55 precursor - pig

ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig

DATE 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999

ACCESSIONS JC4302; PC4093

REFERENCE Suter, B.; Pauli, U.

#authors Gene (1995) 163:263-266

#journal Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

#cross-references MIMD:96011645

#accession JC4302

#molecule_type mRNA

#residues 1-461 ##label SU7

#cross-references GB:U19994; NID:G1141752; PIDN:AA4849.1; PID:G1141753

#accession PC4093

#molecule_type protein

#residues 1-7 ##label SU2

#experimental_source kidney cell line 15

GENETICS

#gene tnfr

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

glycoprotein; kidney; receptor; transmembrane protein; tumor

FEATURES

KEYWORDS 1-79

30-461

44-194

44-82

84-126

211-231

361-447

54,145,151

SUMMARY

Query Match 12.2%; Score 398; DB 2; Length 461;

Best Local Similarity 32.3%; Pred. No. 2,936-53;

Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

Db 33 HPGRREKRESICPGKYSHPONRSICCTCKHGYVLANDCLPGLDTCRCDCNGSTFAS 92

36 OGGRSBR-CDCA-GDF-HKKIGLFCRCGCPAGHYLKAPECTEPGNSICLVCPDPTFLAW 92

QY 93 ENHL-TQCLSSKRSKRSQVEISPCYVDRDTCGCRKN---QYR-KY-WSETLF-Q-C 143

93 ENHNSRCARQACDEQSAVALENCASVADTRCGCKPGWFECCVSCVSSSPFYCOPC 152

Db 144 LNC-SLCPNGTVQPLCKEODTICN-CHSGFLRDKCEVCVNCNADCKNLCPATSETR 201

QY 153 LDGALNRH-T-RLLC-SRRTDCGTCIPGFYEHNDGCVSCTSLSGCPRECAVCGMR 209

Db 202 NDFODGTGTVLLPLVIFEGICLAFLLFVGLACRYQ-R-WPKLYSLTIGCKSPVKEDEBP 260

QY 210 QMEW---VOVLLA-----GLVVPILLGATLTYTHHCWPHK--PLV---TA-DEAGMEA 254

Db 261 LATPSPGPTTTFSPISFSTPTTFSPVSPSSPSTPTTCODMWNINVTSPKRIAPP 320

QY 255 L-TTP---PATHTSPIDS-AHTL-LAPDSSSEKICTQVLGVNSWTP---GYPTQDALCP 305

Db 321 OGAGPLUPMPASPVPPTPLPKMGSAHSAHAPADLADADPATLAVVDGVPPTMKEF 380

QY 306 QVWTSWQOLP-SRALGPAAPTL--SPESPAGSAMMLQBPQ-LYDMDAVPARMKKEF 361

Db 381 VRRILSEHEIERLELNGRCLEAOYSMLAEWRRRTSRREATLELLGSLVRLDGLCL 440

QY 362 VRTIGLREAEIEAVEVEIGR-FRDOQYEMLKRWRQO--QP-AGLGAVYALALERMGLDGCV 417

Db 441 EDIEAL-RGP 450

QY 418 EDLRSRLQRP 428

RESULT 4

ENTRY 157826 #type complete

TITLE tumor necrosis factor receptor - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

ACCESSIONS 157826

REFERENCE 157826

#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Stelmetz, M.

#journal Mol. Immunol. (1993) 30:165-176

#title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

#cross-references MIMD:93156721

#accession 157826

#molecule_type DNA

#status preliminary; translated from GB/EMBL/DBJ

#residues 1-454 ##label RES

#cross-references GB:M76656; NID:G202100; PIDN:AAA40465.1; PID:G202102

GENETICS

#gene TNFR-2

#introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

KEYWORDS cytokine receptor

FEATURE 44-82

SUMMARY

Query Match 11.8%; Score 385; DB 2; Length 454;

Best Local Similarity 28.5%; Pred. No. 1,096-50;

Matches 118; Conservative 79; Mismatches 183; Indels 34; Gaps 28;

Db 40 RDSLCP-OGKYVHKNNSICCTCKHGYVSDCPSPGRDYCRCEKGTFTASNYLR- 97

QY 40 RSPRCDCAGDF-HKKIGLFCRCGCPAGHYLKAPECTEPGNSICLVCPDPTFLAMENHNS 98

Db 98 QCLSKTKRKESQVEISPCQADKDTVCCKENQFORLYSETHFQCVDCSPCFNGTVTIP 157

QY 99 ECARQACDEQSAVALENCASVADTRCGCKPGWFEV-EC-QVSSSP-FYCOPCID 154

Db 158 CKETO-NTVCNCHAGFLRESECVPC--SHCKKNECKMLCLPPLANTYNQDSITAVL 214

QY 155 CGALHRHTRLIC-SR---RDTDCGTCIPGFYEHNGCVS-CPTSLTSGC--PERCAAVCG 207

Db 215 LPLVILGLICLSIFISFISIMCKRYPRMRPREVYSIICRDPV-VKEEKAK-PLTPAPSPAF 272

QY 208 WRQMFVVOY-LIAGLVPLL-LGATL-TYTYRH-CWPHKPLVTADAGMEALTPPATILH 263

Db 273 SPTSGFNPLFGSPGSSPVSTP-ISPIFGPSMWHMPVSEVVPVPGADPLLYESIC 331

QY 264 SPLDS-AHTL-LAPDSSSEKICTQVLGVNSWTPGYPTQDALCPQV-TWSMDQLSRLAG 320

Db 332 SVPAPTSVQKWEDSAHPQPDNADLAILYAVDGYPPAPARKFEMRPMGISEHEIERLEAQ 391

QY 321 PAAAPTLSPSPAGS-PAMMLOPG-POLYDVMDAVPARMKKEFVRTIGLREAEIEAVEVE 378

Db 392 NGRCLEAOYSMLAEWRRRTPRHEDTLEVVGLVSKMNLAGEIENTLEAL-RNP 444

QY 379 IGR-FRDOQYEMLKRWRQOP--AG-LGAVYALALERMGLDGCVEDLRSRLQRP 428

Db	390	HELEERLEONGCIRREAHSMLEAMRRPRRHEATLDVYGRVLCDDMLRGCLNIRETLE	449
QY	370	AEIEAVEVEIGR-FRDOQYEMTKRMROQOP--AGIGAVYAALERMGIDGCVEDLRSRLQ	425
RESULT ENTRY	6	JC2395	#type complete
TITLE		Fas antigen precursor - rat	
ORGANISM		#formal_name Rattus norvegicus #common_name Norway rat	
DATE		20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999	
ACCESSIONS		JC2395; PC2246	
REFERENCE		JC2395	
#authors		Kimura, K.; Wakatsuki, T.; Yamamoto, M.	
#journal		Biochem. Biophys. Res. Commun. (1994) 198:666-674	
#title		A variant mRNA species encoding a truncated form of Fas antigen in the rat liver.	
#cross-references		MUID:94128114	
#accession		JC2395	
#molecule-type		mRNA	
#residues		1-324	#label KIM
#cross-references		DBJ:D26113; NID:g468486; PID:d1005650; PID:g468487	
#experimental_source		thymus	
#accession		PC2246	
#molecule-type		mRNA	
#residues		1-62, 'RFT'	#label K12
#cross-references		DBJ:D26113; NID:g468488; PID:d1005651; PID:g468489	
#experimental_source		liver	
GENETICS			
#introns		62/1	
CLASSIFICATION		transmembrane protein	
KEYWORDS		superfamily NCF receptor repeat homology	
FEATURE			
1-21		#domain signal sequence	#status predicted #label SIG\
22-324		#product Fas antigen	#status predicted #label MAT\
44-79		#domain NCF receptor repeat homology	#label NCF\
81-124		#domain NCF receptor repeat homology	#label NG4\
171-188		#domain transmembrane	#status predicted #label TM\
SUMMARY		#length 324	#molecular_weight 36835 #checksum 7305
Query Match		6.5%;	Score 211; DB 2; Length 324;
Best Local Similarity		30.1%;	Pred. NO. 7.50e-18;
Matches		37; Conservative	26; Mismatches 47; Indels 13; Gaps 12;
Db	43	NCESELIYQ-VGPFCCOPCPGERKYKD-CTTSGAPTCHPCTGEEYTDK-KHYSDCKR	99
QY	45	DCAGPFHKIKIGLFCRCRCAG-HYKAPCTPCGNSCTLCVPCQ-DTFLANDHNHNSCAR	102
Db	100	CAFCDEGHGLEVE-TNCTFRONTKCRCKENFY--CNASLDC-DHC-YHCTSCGLE-DILEP	153
QY	103	COACDE-QASVALLENCASVADTRCGCKPGMFVEQVSGCVSSPFYCPQC-LDCGALHR	160
Db	154	CTR 156	
QY	161	HTR 163	
RESULT ENTRY	7	A46484	#type complete
TITLE		apoptosis-mediating membrane-associated polypeptide Fas - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999	
ACCESSIONS		A46484; A47254	
REFERENCE		A46484	
#authors		Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, N.A.; Nagata, S.	
#journal		J. Immunol. (1992) 148:1274-1279	
#title		The CDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.	
#cross-references		MUID:92148151	
#accession		A46484	

```

##status      preliminary
##molecule_type mRNA
#residues     1-327 ##label WAT
#crosso-references GB:M83649; NID:g193225; PID:g193226
#experimental_source BAM3 macrophage cell line
#note         sequence extracted from NCBI backbone (NCBIN:81544,
               NCBI:P:81545)
REFERENCE
#authors      A47254
#journal      Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
#title        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
               Aberrant transcription caused by the insertion of an early
               transposable element in an intron of the Fas antigen gene
               of lpr mice.
#cross-references MUID:93189576
#accession    A47254
##status      preliminary
##molecule_type nucleic acid
#residues     1-96 ##label ADA
#crosso-references GB:S56490; NID:g298505; PID:g298506
#experimental_source MRI, lpr/lpr
#note         sequence extracted from NCBI backbone (NCBIN:126850,
               NCBIN:126853, NCBIN:126863, NCBI:P:126864)
CLASSIFICATION
KEYWORDS      #superfamily NCF receptor repeat homology
FEATURE       transmembrane protein
44-79         #domain NCF receptor repeat homology #label NGF\
81-124        #domain NCF receptor repeat homology #label NG4
SUMMARY       #length 327 #molecular-weight 37417 #checksum 8479

Query Match   6.28; Score 204; DB 2; Length 327;
Best Local Similarity 27.98; Pred. No. 1.26e-16;
Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;

Db 43 NCSEGIYOG-GPFCOCPQOPGKKRVDDCKKMGSTPTCAPCTEGKEYMD-KNHVADKCRCR 100
.: : : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 45 DCAGDFHKIKIGFCGCGCAGHLYAKPCITPCGNSITCLVGPQDT-FLAMENHHNSECARC 103
| | | : : | : : | | | | : : | : | : | : | : | : | : | : | : | : | :
Qy 104 QACDEQASQVALENCSAVADTRCGCKRPGWFEQOVVS-QCVSSSP 146
| | | : : | : : | | | | : : | : | : | : | : | : | : | : | : | : | :

RESULT      8
ENTRY       137383 #type complete
TITLE       FAS soluble protein - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
            02-Jul-1996
ACCESSIONS 137383
REFERENCE   137383
#authors    Gasclino, I.; Finucci, G.; Papoff, G.; Ruberti, G.
#journal    J. Immunol. (1995) 154:2706-2713
#title      Three functional soluble forms of the human
            apoptosis-inducing Fas molecule are produced by alternative
            splicing.
#cross-references MUID:95181785
#accession  137383
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
#residues   1-314 ##label RES
#crosso-references EMBL:Z47993; NID:g728578; PID:g695539
SUMMARY     #length 314 #molecular-weight 35386 #checksum 655

Query Match  5.88; Score 190; DB 2; Length 314;
Best Local Similarity 34.18; Pred. No. 3.26e-14;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

Db 56 GOFCRHPPCPPE-RKRARDGVNGDEDPVCVOEKEKETD-KAHPSKCRRCRLCDEGHGL 113
| | | : | | : | | | : | : : | : : | : | : | : | : | : | : | :
Qy 55 GLFCCGCCGAGHTLKAP-CIEPCGNSTCLVCPQDT-FLAMENHHNSECARQACDF-QAS 111
.: : | | : : | | | | : : | : | : | : | : | : | : | : | : | : | :
Db 114 EVEI-NCTRTPONTCKRCRKNPFCSNVCEHC 143
.: : | | : : | | | | : : | : | : | : | : | : | : | : | : | : | :

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OY      112 QVALENCASVADTRCGCKPGWFEVQGV5-QC 141
RESULT      9
ENTRY
TITLE      A40036 #type complete
ALTERNATE_NAMES
ORGANISM    apoptosis-mediating surface antigen Fas precursor - human
DATE        surface antigen APD-1
#formal_name Homo sapiens #common_name man
17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
10-Sep-1997
ACCESSIONS
REFERENCE
#authors    A40036; S24543; A38142
#journal     A40036
#title       Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima,
S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.
The polypeptide encoded by the cDNA for human cell surface
antigen Fas can mediate apoptosis.
#cross-references MIMD:91309137
#accession   A40036
#status      preliminary
#molecule_type mRNA
#residues    1-335 #label ITO
#cross-references GB:M67454; NID:g182409; PID:g182410
REFERENCE
#authors     S24543
#submission  submitted to the EMBL Data Library, February 1992
#accession   S24543
#status      preliminary
#molecule_type mRNA
#residues    1-335 #label KRA
#cross-references EMBL:X63717; NID:g28741; PID:g28742
REFERENCE
#authors     A38142
Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.;
Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauttl,
B.C.; Ponstingl, H.; Krammer, P.H.
J. Biol. Chem. (1992) 267:10709-10715
Purification and molecular cloning of the APO-1 cell surface
antigen, a member of the tumor necrosis factor/nerve growth
factor receptor superfamily. Sequence identity with the Fas
antigen.
#cross-references MIMD:92268122
#accession   A38142
#status      preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues    1-134, O',136-335 #label OEH
#experimental_source SKW6.4 cells
#note        sequence extracted from NCBI backbone (NCBIP:103810)
in NCBI backbone the source is designated as mouse
#note
GENETICS
#gene        GDB:APT1
#cross-references GDB:132671; OMIM:134637
#map_position 10q24.1-10q24.1
CLASSIFICATION
KEYWORDS     #superfamily NGF receptor repeat homology
apoptosis; surface antigen; transmembrane protein
FEATURE
1-16         #domain signal sequence #status predicted #label SIG
85-128       #domain NGF receptor repeat homology #label NG4\
174-190      #domain transmembrane #status predicted #label TMM
SUMMARY
#length 335 #molecular_weight 37732 #checksum 4699
Query Match      5.8%; Score 190; DB 2; Length 335;
Best local Similarity 34.1%; Pred. No. 3,26-14;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;
Db      56 GOFCHKPPCPPEG-RKARDCVTNGDEPDPCVQCSKETTD-KAHFSSKCRRCRLCDEBGL 113
111 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
OY      55 GTFCCGCGPAGHLYKAP-CIEPCGNSYCIACPDPT-FLAMENHNHNSCARGCQACDE-QAS 111
111 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
Db      114 EWEI-NCTRTQNTCKRCRKNFCNSTRJCEHC 143
111 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
OY      112 QVALENCASVADTRCGCKPGWFEVQGV5-QC 141

```

RESULT	10	
ENTRY	QGVZML	#type complete
TITLE	T2 protein - myxoma virus (strain Lausanne)	
ORGANISM	#formal_name myxoma virus	
DATE	31-Dec-1992	#text_change 18-Jun-1999
ACCESSIONS	A40566	
REFERENCE	A40566	Upton, C.; Maceen, J.L.; Schreiber, M.; Mcfadden, G.
#authors	#journal	Virology (1991) 184:370-382
#title		Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence.
#cross-references	MUID:91335768	
#accession	A40566	
#molecule_type	DNA	
#residues	1-326	#label UPT
#cross-references	GB:M95181; GB:M7976; NID:g332309; PIDN:AAA46632.1;	
CLASSIFICATION	PID:g933210	#superfamily myxoma virus T2 protein; NGF receptor repeat homology
KEYWORDS	glycoprotein	
FEATURE		
64-105	#domain NGF receptor repeat homology	#label NG2\
106-147	#domain NGF receptor repeat homology	#label NG3\
66,181,205,238	#binding_site carbohydrate (Asn) (covalent)	#status predicted
SUMMARY	#length 326	#molecular_weight 35208 #checksum 9255
Query Match	5.6%; Score 182; DB 1; Length 326;	
Best Local Similarity	30.9%; Pred. No. 7,40e-13;	
Matches	34; Conservative 23; Mismatches 45; Indels 8; Gaps 8;	
Db	5 TLLAYVACVYGAGAPYAGDRGKCRGNDYERDGL-CCTSCPPGYSARLCG-PCSDPVS 62	
QY	25 ALLLVILGARAGQGT-R-SP-RCDAGDPHKIGLFCRCRGCPAGHYLKAPTEPCGNSTCL 82	
Db	63 PCKNETFTA-STNHAAPACVSCRGHCTGLSE-S-QSCDKTRIDRYDCSAG 109	
QY	83 VCPDPTFLAMENHHNSECARCOA-CDBOASQVALENCSSAVALDFRCGCKP 131	
RESULT	11	
ENTRY	D36858	#type complete
TITLE	gene G4R protein - variola virus	
ALTERNATE_NAMES	B28R protein (COP)	
ORGANISM	#formal_name variola virus	
DATE	30-Sep-1993	#sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
ACCESSIONS	D36858; S46888; S32385; S35987	
REFERENCE	A36859	
#authors	Blinov, V.M.	
#submission	submitted to Genbank, November 1992	
#description	not shown.	
#accession	D36858	
#status	preliminary	
#molecule_type	DNA	
#residues	1-349	#label BLI
#cross-references	GB:X69198; NID:g456758; PID:g457087	
REFERENCE	S46868	##experimental_source strain India1967, ssp. major, isolate Ind3
#authors	Kolykhalov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sandachchiev, L.S.	
#submission	submitted to the EMBL data library, April 1992	
#description	Nucleotide sequence analysis of the region of variola virus XhoI F O H P Q genome fragment.	
#accession	S46888	
#status	preliminary	
#molecule_type	DNA	
#residues	1-349	#label KOL
#cross-references	EMBL:X67117; NID:g516428; PID:g516449	
#experimental_source	strain India1967, isolate Ind3	

```

REFERENCE      S32385
#authors      Shchelkunov, S.N.; Blinov, V.M.; Sandakchiev, L.S.
#journal      FEBS Lett. (1993) 319:80-83
#title        Genes of variola and vaccinia viruses necessary to overcome
              the host protective mechanisms.
#cross-references MUID:93202281
#accession    S32385
#molecule_type DNA
#residues     31-168 #label SHC
##cross-references EMBL:X69198
##experimental_source strain India-1967, ssp. major

GENETICS
#gene         G4R
CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat
               homology

FEATURE
#32-66        #domain NGF receptor repeat homology #label NGF\
68-109        #domain NGF receptor repeat homology #label NG2\
110-151       #domain NGF receptor repeat homology #label NG3
SUMMARY
Query Match   5.5%; Score 179; DB 2; Length 349;
Best Local Similarity 27.1%; Pred. NO.2.36e-12;
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7;

Db 15 IINGRDAPPTPPNGKCKDTEY-KRHH-LCCLSCPGTYASRLC-DSKTNTOCTPCGSG 71
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Oy 29 VLLGARAGGGRSPRCDC-AGDFPKKIKIGLFCCRCGPGHYHLKAPCTPCGNSCTVCPQD 87
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

Db 72 TFTSKNNHL-PACLSGNGRCN-SNOYETNSCNTTHRIECSGIGY 115
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Oy 88 TFLAMENHNSECARCOA-CDEQASOALENCASAVADTRCGCKPGWF 133
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

RESULT 12
ENTRY   A46517 #type complete
TITLE   CD27 antigen precursor - human
ALTERNATE_NAMES CD27L receptor; T cell activation antigen CD27
ORGANISM Homo sapiens #common.name man
DATE    18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change
        22-Jun-1999

ACCESSIONS
REFERENCE A46517
#authors  Loeenen, W.A.; Gravaestein, L.A.; Beumer, S.; Meljef, C.J.;
          Hagemeijer, A.; Borst, J.
#journal  J. Immunol. (1992) 149:3937-3943
#title    Genomic organization and chromosomal localization of the
          human CD27 gene.
#cross-references MUID:93094588
#accession A46517
#status    not compared with conceptual translation
#molecule_type DNA
#residues  1-260 #label LOE
#note      sequence extracted from NCBI backbone (NCBI:P120386)
#note      authors propose an alternative repeat pattern
REFERENCE A46454
#authors  Cammerlil, D.; Walz, G.; Loeenen, W.A.; Borst, J.; Seed, B.
#journal  J. Immunol. (1991) 147:3165-3169
#title    The T cell activation antigen CD27 is a member of the nerve
          growth factor/tumor necrosis factor receptor gene family.
#cross-references MUID:92013149
#accession A46454
#molecule_type mRNA
#residues  1-58, 'A', 60-260 #label CAM
#cross-references GB:M63928; NID:9180084; PTDN:AA58411.1; PID:g1800855
#note      sequence extracted from NCBI backbone (NCBIN:60285,
          NCBI:P:60289)

COMMENT      A soluble CD27 found in serum and urine is formed by proteolysis.
GENETICS
#gene         GDB:CD27
#cross-references GDB:132582; OMTM:186711
#map_position 12p13-12p13
#introns     46/1; 90/1; 150/1; 180/1; 220/1

```

CLASSIFICATION #superfamily CD27 antigen; NGF receptor repeat homology
KEYWORDS duplication; glycoprotein; homodimer; phosphoprotein;
receptor; surface antigen; T-cell; transmembrane protein

FEATURE

1-20 #domain signal sequence #status predicted #label SIG
21-260 #product CD27 antigen #status predicted #label MAT
21-191 #domain extracellular #status predicted #label EXT
27-63 #domain NGF receptor repeat homology #label NG1
65-105 #domain NGF receptor repeat homology #label NG2
121-188 #region proline/serine/threonine-rich
192-211 #domain transmembrane #status predicted #label TMN
212-260 #domain intracellular #status predicted #label INT
95 #binding-site carboxylate (Asn) (covalent) #status
predicted

SUMMARY #length 260 #molecular-weight 29186 #checksum 1652

Query Match 5.4%; Score 177; DB 1; Length 260;

Best Local Similarity 25.2%; Pred. No. 5,09e-12;

Matches 32; Conservative 36; Mismatches 50; Indels 9; Gaps 7;

Db 4 PHEWMLCVLTGLSTAPRK-SCPERHWAGKLCQMCPEPTLVKODQHRKTAQC 62

Oy 23 PQALLLVLLGA-RAQGTSPRCDCAGDFHKRTGLFCRCGPAGHYLAKPCTPCGNSYC 81

Db 63 DPCIPGVSP-DHHTPHCESRHCN--SGLL-VRNCTITANECACRNGM--QCRDKE 116

Oy 82 LVC-PQDTFLAMENHNHSEACRCACDEQASQVALENCSAVADTRCGCKPWFVEQVSO 140

Db 117 CTRECDPL 123

Oy 141 CVSSSP 147

RESULT 13
ENTRY S12783 #type complete
TITLE OX40 antigen precursor - rat
ALTERNATE_NAMES nerve growth factor receptor homolog
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
20-Sep-1999

ACCESSIONS S12783; S08036
REFERENCE S12783
#authors Mallett, S.; Fossum, S.; Barclay, A.N.
#journal EMBO J. (1990) 9:1063-1068
#title Characterization of the MRC OX40 antigen of activated CD4
positive T lymphocytes - a molecule related to nerve growth
factor receptor.

#cross-references MIMD:90214614
#accession S12783
#molecule_type mRNA
#residues 1-271 #label MAL
#cross-references EMBL:X17037; NID:957830; PID:957831
CLASSIFICATION #superfamily CD27 antigen; NGF receptor repeat homology
KEYWORDS growth factor receptor; transmembrane protein
FEATURE 1-19 #domain signal sequence #status predicted #label SIG
20-271 #product OX40 antigen #status predicted #label MAT
211-235 #domain transmembrane #status predicted #label TMN
SUMMARY #length 271 #molecular-weight 29895 #checksum 379

Query Match 5.1%; Score 165; DB 2; Length 271;

Best Local Similarity 29.7%; Pred. No. 4.82e-10;

Matches 22; Conservative 17; Mismatches 32; Indels 3; Gaps 3;

Db 37 CCRECGHGMVSGC-DHTRTVCHPC-EPGFYN-EAVNYDTCKOCTCNHRSGSELMON 93

Oy 58 CCRCPAGHYLAKPCTPCGNSYGLVCPQDTFLAMENHNHSEACRCACDEQASQVALEN 117

Db 94 CTPTEDTVCOCRPG 107

Oy 118 CSAVADTRCGCKPG 131

RESULT 14

ENTRY 148700 #type complete

TITLE gene ox40 protein - mouse

ALTERNATE_NAMES OX40 antigen

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
18-Oct-1996

ACCESSIONS 148700; 148334; S34377

REFERENCE 148700

#authors Calderhead, D.M.; Buhlmann, T.E.; van den Eertwegh, A.J.;

#journal J. Immunol. (1993) 151:5261-5271

#title Cloning of mouse OX40: a T cell activation marker that may
mediate T-B cell interactions.

#cross-references MIMD:94044750

#accession 148700

#status translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-272 #label RES

#cross-references EMBL:221674; NID:g312827; PID:g312828

REFERENCE 148334

#authors Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins,

#journal Eur. J. Immunol. (1995) 25:926-930

#title Gene structure and chromosomal localization of the mouse
homologue of rat OX40 protein.

#cross-references MIMD:95255413

#accession 148334

#status translated from GB/EMBL/DBJ

#molecule_type DNA

#residues 1-14, G, 16-272 #label RE2

#cross-references EMBL:X85214; NID:g732818; PID:g732819

GENETICS

#gene ox40

#introns 45/1; 86/1; 122/1; 144/2; 210/1; 250/1

SUMMARY #length 272 #molecular-weight 30153 #checksum 841

Query Match 5.1%; Score 167; DB 2; Length 272;

Best Local Similarity 30.0%; Pred. No. 2.27e-10;

Matches 33; Conservative 22; Mismatches 49; Indels 6; Gaps 6;

Db 5 VOQPTALLL-ALITGVN-ARLNCVKHTYPS-GHKRCRCQPGHGMVSGC-DHTRDTLC 60

Oy 22 VQALLLVLLGARAQGTSPRCDCAGDFHKRTGLFCRCGPAGHYLAKPCTPCGNSYC 81

Db 61 HPC-ETGFYN-EAVNYDTCKOCTCNHRSGSELMONCTPTOYVCRPG 108

Oy 82 LVC-PQDTFLAMENHNHSEACRCACDEQASQVALENCSAVADTRCGCKPG 131

RESULT 15

ENTRY A35356 #type complete

TITLE tumor necrosis factor receptor type 2 precursor - human

ALTERNATE_NAMES 75K tumor necrosis factor receptor

ORGANISM #formal_name Homo sapiens #common_name man

DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999

ACCESSIONS A35356; A48416; A36007; A23666; B35010; I38094

REFERENCE A35356

#authors Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann,

#journal M.P.; Jerzy, R.; Dower, S.K.; Cosman, D.; Goodwin, R.G.

#title Science (1990) 248:1019-1023

#title A receptor for tumor necrosis factor defines an unusual
family of cellular and viral proteins.

#cross-references MIMD:90260639

#accession A35356

#status preliminary

#molecule_type mRNA

#residues 1-461 #label SWI

#cross-references GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186

REFERENCE A36475

#authors Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King,

M.W.; Hale, K.K.; Squires, C.H.; Thompson, R.C.; Yarnice,


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#journal      J.L.
#title        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8331-8335
#cross-references MUID:91045991
#accession    A36475
#status       preliminary
##molecule_type mRNA
##residues    1-195,'R',197-461 ##label KOH
#cross-references GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1;
#accession    A48416
#status       preliminary
##molecule_type mRNA; protein
##residues    23-461 ##label DBM
#cross-references GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
#note         sequence extracted from NCBI backbone (NCBIN:63368,
#             NCBI:P:63371)
REFERENCE
#authors      Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang,
#journal      D.; Ringold, G.M.
#title        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
#cross-references MUID:90349572
#accession    A36007
#status       preliminary
##molecule_type mRNA
##residues    116-140,'P',142-195,'R',197-362,'T',364-461 ##label HBL
#cross-references GB:M35857; NID:9339751; PIDN:AAA63262.1; PID:9339752
REFERENCE
#authors      Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.;
#journal      Lesslauer, W.; Brockhaus, M.
#title        J. Biol. Chem. (1990) 265:20131-20138
#cross-references MUID:91056448
#accession    A23666
#status       preliminary
##molecule_type protein
##residues    23-40;65-69;136-141;300-306 ##label LOE
REFERENCE
#authors      Engelmann, H.; Novick, D.; Wallach, D.
#journal      J. Biol. Chem. (1990) 265:1531-1536
#title        Two tumor necrosis factor-binding proteins purified from
#             human urine. Evidence for immunological cross-reactivity
#             with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession    B35010
#status       preliminary
##molecule_type protein
##residues    27-31 ##label ENG
REFERENCE
#authors      Kuhnert, P.; Kemper, O.; Wallach, D.
#journal      Gene (1994) 150:381-386
#title        Cloning, sequencing and partial functional characterization
#             of the 5' region of the human p75 tumor necrosis factor
#             receptor-encoding gene (TNF-R).
#cross-references MUID:95121934
#accession    I38094
#status       preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-37 ##label RES
#cross-references EMBL:X80021; NID:9666044; PIDN:CAA56324.1;
#accession    PID:9825701
GENETICS

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#gene          GDB:TNFR2
##cross-references GDB:125914; OMIM:191191
#map_position  1p36.2-1p36.2
#introns       26/3
#note          the list of introns is incomplete
CLASSIFICATION #superfamily tumor necrosis factor receptor type 2; NGF
#receptor repeat homology
FEATURE        duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE        1-22
#domain signal sequence #status predicted #label Sig\
#product tumor necrosis factor receptor type 2 #status
#experimental #label MAT\
40-76          #domain NGF receptor repeat homology #label NG1\
78-119         #domain NGF receptor repeat homology #label NG2\
120-162        #domain NGF receptor repeat homology #label NG3\
164-201        #domain NGF receptor repeat homology #label NG4\
262-279        #domain transmembrane #status predicted #label TMN\
280-461        #domain intracellular #status predicted #label INT\
171,193        #binding site carbohydrate (Asn) (covalent) #status
#predicted
SUMMARY        #length 461 #molecular-weight 48291 #checksum 5724
Query Match    5.1%; Score 168; DB 1; Length 461;
Best local Similarity 27.6%; Pred. No. 1.56e-10;
Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;
Db             44 EYDQTAQMCCKSCSPQAHAKVFCTKT-SPTVCDSCEDSTYTQIW-NW-VPECLSCGSRG 100
               :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy             49 DFHKKIGLFCCRCRCPAGHYLKAPECTEPCGNSCLVCPQDFLA-WENHNNSECARCOA-C 106
               ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db             101 S--SDQYETQACTREQNRICTCRPGWY 125
               ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy             107 DEQASQVALENCSAVADTRCGCKRPGWF 133
               ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Search completed: Tue Jul 25 22:21:58 2000
Job time : 27 secs.

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DB 244 ALTPRATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTPGVPEIOEALCPQVTSMDQ 303
    |||
OY 254 ALTPRATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTPGVPEIOEALCPQVTSMDQ 313
DB 304 LPSRALGPAAPLTPSPSPAGSPAMMLQPGPOLYDVMDAPARRMKEFEVTLGLREAIE 363
    |||
OY 314 LPSRALGPAAPLTPSPSPAGSPAMMLQPGPOLYDVMDAPARRMKEFEVTLGLREAIE 373
DB 364 AVEVEIGRFDOOYEMLKRRQOOPALGAVYALERMGLDGCVEDLRSRLQRP 418
    |||
OY 374 AVEVEIGRFDOOYEMLKRRQOOPALGAVYALERMGLDGCVEDLRSRLQRP 428

RESULT 2
ID 014865 PRELIMINARY; PRT; 426 AA.
AC 014865;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE DEATH RECEPTOR 3 BETA.
GN DR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98113360.
RA WARZOGHA K., RIBEIRO P., CHARLOT C., RENARD N., COIFFIER B.,
RA SALLES G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas."
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
EMBL: AF026070; AAC39556.1; -.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PFAM: PF00531; death; 1.
DR PFAM: PF00202; TNFR_c6; 2.
SQ SEQUENCE 426 AA; 45950 MW; 87E00821 CRC32;

Query Match 87.7%; Score 2865; DB 4; Length 426;
Best Local Similarity 92.4%; Pred. No. 0.00e+00;
Matches 391; Conservative 11; Mismatches 12; Indels 9; Gaps 5;
DB 4 RPRCAVAALLLVLLGARAOGGTRSPRCAGDFHKKIGFCRCGCPAGHYLKAPCTE 63
    |||
OY 15 RGSAAAVPQALLVLLGARAOGGTRSPRCAGDFHKKIGFCRCGCPAGHYLKAPCTE 74
DB 64 PCGNSTGLVCPQDTFLAMENHNHSEACARQACDEQASQVALENCASAVADTRCGCKPGWV 123
    |||
OY 75 PCGNSTGLVCPQDTFLAMENHNHSEACARQACDEQASQVALENCASAVADTRCGCKPGWV 134
DB 124 ECVYSCVSSSPFYCQPLDGCALHRTLRILCSRDTCCGCTLPFGYEHGDCVSCPTRP 183
    |||
OY 135 ECVYSCVSSSPFYCQPLDGCALHRTLRILCSRDTCCGCTLPFGYEHGDCVSCPTRP 193
DB 184 PSLAGAPGAVOSVPLSVAGRGVFNVOYLLAGLVPLLLGATLTYTRCMPHKKPL 243
    |||
OY 194 -TLSSCP--E-RCA---AVCGMR-OMFNVOYLLAGLVPLLLGATLTYTRCMPHKKPL 245
DB 244 TADAGMGAALTPRATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTPGVPEIOEALCP 303
    |||
OY 246 TADAGMGAALTPRATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTPGVPEIOEALCP 305
DB 304 QVTSMWDLPSRALGPAAPLTPSPSPAGSPAMMLQPGPOLYDVMDAPARRMKEFEVTL 363
    |||
OY 306 QVTSMWDLPSRALGPAAPLTPSPSPAGSPAMMLQPGPOLYDVMDAPARRMKEFEVTL 365
DB 364 GLREAIEAVEVEIGRFDOOYEMLKRRQOOPALGAVYALERMGLDGCVEDLRSRLQ 423
    |||
OY 366 GLREAIEAVEVEIGRFDOOYEMLKRRQOOPALGAVYALERMGLDGCVEDLRSRLQ 425
DB 424 RGP 426

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OY 426 RGP 428
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RESULT 3
ID 000279 PRELIMINARY; PRT; 372 AA.
AC 000279;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 8
DE (LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX SKEATON G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,
RA BELL J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U94509; AAC51314.1; -.
DR EMBL: U94506; AAC51311.1; -.
DR HSSP: P19438; 1TNR.
DR PFAM: PF00531; death; 1.
DR KW Alternative splicing.
SQ SEQUENCE 372 AA; 40391 MW; 430DA0D5 CRC32;

Query Match 75.0%; Score 2451; DB 4; Length 372;
Best Local Similarity 98.5%; Pred. No. 0.00e+00;
Matches 321; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
DB 48 CRGCPA-ASQVALENCASAVADTRCGCKPGWFEQVSCVSSSPFYCQPLDGCALHRT 106
    |||
OY 103 COACDEQASQVALENCASAVADTRCGCKPGWFEQVSCVSSSPFYCQPLDGCALHRT 162
DB 107 RLCSRDTCCGCTLPFGYEHGDCVSCPTSTLSCPECAVCGMRQVVOYLLAGLV 166
    |||
OY 163 RLCSRDTCCGCTLPFGYEHGDCVSCPTSTLSCPECAVCGMRQVVOYLLAGLV 222
DB 167 VLLLGATLTYTRCMPHKKPLVTADAGMGAALTPRATHSLPDSAHNTLLAPPDSSEK 226
    |||
OY 223 VLLLGATLTYTRCMPHKKPLVTADAGMGAALTPRATHSLPDSAHNTLLAPPDSSEK 282
DB 227 CTVOLVGNSTPGVPEIOEALCPQVTSMDQLPSRALGPAAPLTPSPSPAGSPAMMLQ 286
    |||
OY 283 CTVOLVGNSTPGVPEIOEALCPQVTSMDQLPSRALGPAAPLTPSPSPAGSPAMMLQ 342
DB 287 GPOLYDVMDAPARRMKEFEVTLGLREAIEAVEVEIGRFDOOYEMLKRRQOOPAGIG 346
    |||
OY 343 GPOLYDVMDAPARRMKEFEVTLGLREAIEAVEVEIGRFDOOYEMLKRRQOOPAGIG 402
DB 347 AVYAALERMGLDGCVEDLRSRLQRP 372
    |||
OY 403 AVYAALERMGLDGCVEDLRSRLQRP 428

RESULT 4
ID 000280 PRELIMINARY; PRT; 380 AA.
AC 000280;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97272273.
RX SKEATON G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
RA MCMICHAEL A.J., BELL J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing."

```

RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 DR EMBL: U94510; AAC51315.1; -.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PFAM: PF00531; death; 1.
 DR PFAM: PF00020; TNFR_C6; 2.
 SQ SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;

Query Match 73.6%; Score 2403; DB 4; Length 380;
 Best Local Similarity 89.1%; Pred. No. 0.00e+00;
 Matches 369; Conservative 4; Mismatches 4; Indels 37; Gaps 1;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74
 Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 123
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 134
 Db 124 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 183
 135 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 194
 Db 184 LGSCPERCAAVCGMRQ-----NEAGMEA 206
 195 LGSCPERCAAVCGMRQWQVLLAGLVPLLLGATLTYTRHGWPKPLVTADAEAMEA 254
 Db 207 LTPPATHLSPDLSAHTLAPDPSSEKICTVQLVGNSTPGYPTGTCALCPQVTWMDQL 266
 255 LTPPATHLSPDLSAHTLAPDPSSEKICTVQLVGNSTPGYPTGTCALCPQVTWMDQL 314
 Db 267 PSRATGPAAPRTSPSPAGSPAMMLOPQPOLYDMADAVARRKKEFVRLGLEAEIEA 326
 315 PSRATGPAAPRTSPSPAGSPAMMLOPQPOLYDMADAVARRKKEFVRLGLEAEIEA 374
 Db 327 VEVEIGFRDQOYEMLRKMRQOPAGIGAVYALERMGLDGCVDLRSRLQRP 380
 375 VEVEIGFRDQOYEMLRKMRQOPAGIGAVYALERMGLDGCVDLRSRLQRP 428

RESULT 5
 ID 000276 PRELIMINARY; PRT; 253 AA.
 AC 000276;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97272273.
 RA SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
 RA MCHICHAEL A.J., BELL J.I.;
 RT "LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 DR EMBL: U94503; AAC51308.1; -.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PFAM: PF00020; TNFR_C6; 2.
 SQ SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;

Query Match 45.8%; Score 1497; DB 4; Length 253;
 Best Local Similarity 95.5%; Pred. No. 0.00e+00;
 Matches 190; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74

Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 123
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 134
 Db 124 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 183
 135 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 194
 Db 184 LGSCPERCAAVCGMRQW 202
 195 LGSCPERCAAVCGMRQW 213

RESULT 6
 ID 014866 PRELIMINARY; PRT; 277 AA.
 AC 014866;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE SOLUBLE DEATH RECEPTOR 3 BETA.
 GN DR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MAZCOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
 RA SALES G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026071; AAB82288.1; -.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PFAM: PF00020; TNFR_C6; 2.
 SQ SEQUENCE 277 AA; 29111 MW; 06E165C7 CRC32;

Query Match 41.1%; Score 1343; DB 4; Length 277;
 Best Local Similarity 95.5%; Pred. No. 1.19e-27;
 Matches 171; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74
 Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 123
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 134
 Db 124 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 182
 135 ECVSSQCVSSSPFYCQPCLDGALHRRTRLCSRRDTCGTCLPGFYEHDGCVSCPTST 193

RESULT 7
 ID 000278 PRELIMINARY; PRT; 234 AA.
 AC 000278;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97272273.
 RA SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
 RA MCHICHAEL A.J., BELL J.I.;
 RT "LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 DR EMBL: U94508; AAC51313.1; -.
 DR PFAM: PF00531; death; 1.
 SQ SEQUENCE 234 AA; 25373 MW; 272FD3C9 CRC32;

Query Match 40.7%; Score 1329; DB 4; Length 234;
 Best Local Similarity 100.0%; Pred. No. 2,14e-268;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 53 ADAGMALPPATHTSPDASHTLAPDPSSSEKICTVOLVGNWMTPGYPTOALCPQ 112
 |||
 QY 247 ADEGEMALPPATHTSPDASHTLAPDPSSSEKICTVOLVGNWMTPGYPTOALCPQ 306
 |||
 Db 113 VTMWMDLPSPALCPAAPTLPSPSPAGSPAMMLQPGPOLYDMDVAVPARRKEFVTLG 172
 |||
 QY 307 VTMWMDLPSPALCPAAPTLPSPSPAGSPAMMLQPGPOLYDMDVAVPARRKEFVTLG 366
 |||
 Db 173 LREAEIAYEVEIGRFDOOYEMLKRRQOCPAGLGAAYALERMGLDGEDLSRLQR 232
 |||
 QY 367 LREAEIAYEVEIGRFDOOYEMLKRRQOCPAGLGAAYALERMGLDGEDLSRLQR 426
 |||
 Db 233 GP 234
 |||
 QY 427 GP 428

RESULT 8
 ID 000277; PRELIMINARY; PRT: 126 AA.
 AC 000277;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97272273.
 RA SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
 RA MCMICHAEL A.J., BELL J.I.;
 RT "IARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 RL EMBL; U94507; AAC51312.1; -;
 DR EMBL; U94507; AAC51312.1; -;
 SQ SEQUENCE 126 AA; 13349 MW; B4B4851A CRC32;

Query Match 14.3%; Score 467; DB 4; Length 126;
 Best Local Similarity 92.2%; Pred. No. 2.63e-72;
 Matches 59; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Db 48 CRGCPA-ASQVLENCASVADTRCGCKRGWVEYECVSSSPYCPCLDGCALHRT 106
 |||
 QY 103 CQACDEQASQVLENCASVADTRCGCKRGWVEYECVSSSPYCPCLDGCALHRT 162
 |||
 Db 107 RLIC 110
 |||
 QY 163 RLIC 166

RESULT 9
 ID 019131; PRELIMINARY; PRT: 471 AA.
 AC 019131;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE Tumor NECROSIS FACTOR-RECEPTOR I.
 GN TNF-R1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-AORTA;
 RA LEE E.-K., TAYLOR M.J., KEHLI M.E.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; U90937; AAB65143.1; -;
 DR HSSP; P19438; 11NR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00020; TNFR_c6; 3.
 SQ SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;

Query Match 8.3%; Score 272; DB 6; Length 471;
 Best Local Similarity 30.0%; Pred. No. 2.91e-31;
 Matches 128; Conservative 79; Mismatches 169; Indels 51; Gaps 34;

Db 40 RESPCP-OGKYNHPONSTICCTCKHGYLYNDGPGPRDTCRCVACGTYALENHLR 98
 |||
 QY 40 RSPRDCAGDF-HKIKGFCCRCGCPAGHYLKPCTEPCGNSCLYCPDFTFLAMENHNS 98
 |||
 Db 99 -CLSSRRDEMFQVEIPCVYDRTVGGCKRQYREW-GE-TGFRCLNCSLCPN-GTY 154
 |||
 QY 99 BCARCQACDEQASQVLENCASVADTRCGCKRGWVEYECVSSSPYCPCLDGCAL 158
 |||
 Db 155 NIPQ---ERODTIC-HCHMGFELKACISCHDCKNECEKICPTPRSTGKSODPGTT 210
 |||
 QY 159 HRTLLCSKRDTCGTCLPGTYEHGDCVSCPTSLGSCPRCAA-VC-GW-RQMFVQ 215
 |||
 Db 211 VLLPLVIFGLCLASFASVYIACRYORMKPKLYSIICGOSTLVKGBPELLVPAGFNPT 270
 |||
 QY 216 VLLAGLVV-PL-LTG-ATLTYTYR-HCWPHK--PLV---T-ADEGEMALP-P---PA 260
 |||
 Db 271 TTICSSSPSSSPVSIPIPIYISCDRNFQAVASPSSETAPHLKAGPILPGPASTHLCPT 330
 |||
 QY 261 THL--SPDASHTLAP-DSEK--ICTVOLVGNWMTPGYPTOALC-PQYTSW-DQ 313
 |||
 Db 331 GPASTHLCPTGPASTHLCPTVQKWEASAPAPDADPATLVAVDGVPSRWKL 390
 |||
 QY 314 -LPSRA-L---GPAAPTL-SP-----ESPA-GSPAMMLQPGH-LYDMDVAVPARRKEF 361
 |||
 Db 391 VRLGISEHEIRLENGRHIREAOYSMLAAMRRTPPREATLGLGVLADMGLGL 450
 |||
 QY 362 VTLGIREAEIAYEVEIGR-FRDOOYEMLKRRQOOP---AGLGAAYALERMGLDGC 417
 |||
 Db 451 ENIEENL 457
 |||
 QY 418 EDLSRL 424

RESULT 10
 ID 097491; PRELIMINARY; PRT: 327 AA.
 AC 097491;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE FAS PROTEIN.
 GN FAS.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCYTE;
 RA TAKAGI M., TAKAHASHI H., KABEYA H., OHASHI K., SUGIMOTO C., ONUMA M.;
 RT "Cloning of sheep fas antigen";
 RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB011671; BAA37093.1; -;
 DR HSSP; P25445; 1DDF.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 SQ SEQUENCE 327 AA; 36928 MW; 67261BB8 CRC32;

Query Match 6.7%; Score 218; DB 6; Length 327;
 Best Local Similarity 30.2%; Pred. No. 1.13e-20;
 Matches 32; Conservative 23; Mismatches 44; Indels 7; Gaps 5;

Db 56 LFCQCPGPKRKNCKCKRDGMPCEVLCSEGEHYTD-KSHSDKICRCVCDENGLGV 114
 |||

OY 56 LFCRCGCPAGHYLKAPCTEPCGNSCLVCPQ-DTFLAMENHNHSECARCQACDEQASOVA 114
Db 115 EHNCRTNONTKCRCKSNF--CNSSPCEHCNP--CTTC-ENGILEK 155
OY 115 LENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGALHR 160

RESULT 11
ID 09Y606 PRELIMINARY: PRT: 616 AA.
AC 09Y606:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE RECEPTOR ACTIVATOR OF NUCLEAR FACTOR-KAPPA B.
GN RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 98032977.
RA ANDERSON D.M., MARASROVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,
RA TOMERSKO M.E., ROUX E.R., TEEPE W.C., DUBOSE R.F., COSMAN D.,
RA GALIBERT L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function."
RL Nature 390:175-179(1997)
DR EMBL: AF018253; AAB86809.1; -.
KW Receptor.
SQ SEQUENCE 616 AA; 66033 MW; 6AF398F8 CRC32;

Query Match 6.5%; Score 213; DB 4; Length 616;
Best Local Similarity 31.0%; Pred. No. 1,01e-19;
Matches 49; Conservative 29; Mismatches 65; Indels 15; Gaps 14;

Db 15 LILCALLARQVALQIAPCTSEKHYEH-LGR-CQNKCEPKYMSKCTTT-SDSVCLPC 71
OY 26 LILVLLGARAAGGTR-SPRCDCAGDFHKRIGLCRCGCPAGHYLKAPCTEPCGNSCLV 84
Db 72 GPDEYLDNM-NEEDK-CLHKVQDTGKALVAVYAGNSTTTRRCACTAG-TMMSDCECCR 128
OY 85 PDQTFI-AMENHNHSECARCQACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCV 143
Db 129 RNT-ECAPGL-GA-O-HPLQL-NK-DTVCKPCLAGYF 159
OY 144 SSPFYCQPCLDGALHRHRLCLSRDTCGTLPGFY 181

RESULT 12
ID 09Y530 PRELIMINARY: PRT: 189 AA.
AC 09Y530:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA DUTHIE S., NASIR L., ARGYLE D.J., ECKERSALL P.D.;
RT "Canine tumor necrosis factor receptor, partial cds."
RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF013955; AAD01516.1; -.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR Receptor.
KW NON_TER 189
FT SEQUENCE 189 AA; 21324 MW; 2AA93BEF CRC32;
SQ SEQUENCE 189 AA; 21324 MW; 2AA93BEF CRC32;

Query Match 6.4%; Score 210; DB 6; Length 189;
Best Local Similarity 31.8%; Pred. No. 3.74e-19;

Matches 47; Conservative 23; Mismatches 66; Indels 12; Gaps 8;
Db 44 CPQGYTHPPDDSTICTCHGKTYLYNDCPGGLDTPDRECNGFTASENHLR-QCLSC 102
OY 46 CA-GDF-HKKIGLFCRCGCPAGHYLKAPCTEPCGNSCLVCPQDPLFLAMENHNHSECARC 103
Db 103 SKCRENMQVEISPTCYVRDVCGRKN---QYRFY--SEPLFCQNNCSLC-LNGTVQ 155
OY 104 QACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGALHRHR 163
Db 156 ISCOEKQNTIC-TCHAGFFLREHCVSC 182
OY 164 LLC-SRDTDCGTLCPGFYEHGDCGVSC 190

RESULT 13
ID 09Y185 PRELIMINARY: PRT: 189 AA.
AC 09Y185:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN (1)
RP SEQUENCE FROM N.A.
RA DUTHIE S., NASIR L., ECKERSALL P.D.;
RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U72344; AAB95089.1; -.
DR HSSP: P19438; 1EXT.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PFAM: PF00020; TNFR_C6; 3.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MW; 687732D2 CRC32;

Query Match 6.3%; Score 206; DB 6; Length 189;
Best Local Similarity 31.8%; Pred. No. 2.12e-18;
Matches 49; Conservative 24; Mismatches 67; Indels 14; Gaps 11;

Db 40 RAIPCP-OGKTYHPDINSICCTKCHKTYLYNDCGPELDTPCRECGNGFTASENYLR- 97
OY 40 RSPDCDCGDP-HKKIGLFCRCGCPAGHYLKAPCTEPCGNSCLVCPQDPLFLAMENHNH 98
Db 98 QCLSCSKCRKMYOYEISPTCYVRDVCGRK---N-QY-RYYWSETHF-Q-CLNCSLC 149
OY 99 ECARCQACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGCA- 157

Db 150 LNTGVQISCKETQNTVC-TCHAGFFLREHCVSC 182
OY 158 LHRHRLCLS-RDPTDCGTLCPGFYEHGDCGVSC 190

RESULT 14
ID 09XS60 PRELIMINARY: PRT: 263 AA.
AC 09XS60:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE PAS ANTIGEN SPLICED VARIANT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN (1)
RP SEQUENCE FROM N.A.
RA ISONO T., TANBE Y., NAGANO Y., SETO A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021297; BAA78429.1; -.
SQ SEQUENCE 263 AA; 30374 MW; 43BF129F CRC32;

Query Match 6.2%; Score 202; DB 6; Length 263;

Best Local Similarity	34.08;	Pred. No. 1.19e-17;
Matches	32; Conservative	19; Mismatches 37; Indels 6; Gaps 5;

Matches	32;	Conservative	19;	Mismatches	37;	Indels	6;	Gaps	5;
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Db 41 GNFCQCLCPPTKKRADTCSNGKRPDCPPCGEGEYTD-KSHFSKCRCRLCDGSEHGLE 99
 | ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Qy 55 GLFCCRGPAGHYLKAPCTEPCCGNSTLCVPC-Q-DFLANENHHNSECARQCACD-EDASQ 112

55 GLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECARCQACD-EQASQ 112

DB 100 VETD-CTTIQNTKCRCKSNFF--CNALKEHCDP 130

113 VALENCASAVADTRCGCKPGWFEVCQVSQCVCSSSP 146

RESULT 15

PRELIMINARY; PRT; 320 AA.

AC Q9XS29

DT 01-NOV-1999 (TREMBLEL, 12, Created)

DT	01-NOV-1999	(TREMBlrel. 12, Last sequence update)
ET	01-NOV-1999	(TREMBlrel. 12, Last annotation update)

DT 01-NOV-1999 (Tremblérel. 12, last annotation update)

DE C-TYPE FAS ANTIGEN

Oryctolagus cuniculus (Rabbit)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Insectomorpha: Lemnoridae: Orvoto]acus

OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
BN [1]

RN	SEQUENCE FROM N. A.
BP	[1]

RP SEQUENCE FROM N.A.
BA TSONO T TANBE Y.

RAISONO F., TANBE Y., NAGANO Y., SEIO A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";

RT -splicing and allelic variation in the rabbit fas antigen gene.
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

KL submitted (DEC-1998) CO line EMBL/GENBANK/DDO accuases
 EMBL; AB021299; BAA78431.1; -
 DR

DR	EMBL; AB021296; BAA78428.1; -.
DR	EMBL; AB021295; BAA78428.1; -.

DN 320 AA; 36102 MW; A1D1D1A1 CRC32;
SEQUENCE

[illegible]

Query Match	6.28; Score 202; DB 6; Length 320;
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Best Local Similarity 34.0%; Pred. No. 1.19e-17;

Matches	32;	Conservative	19;	Mismatches	37;	Indels	6;	Gaps	5;
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Db 41 GNFCCLCPGTTKKADCTSNKGKPDCEPCQEGEETD-KSHFSSKCRCSLCDGEHGLE 99

55 GLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECARCQACD-EQASQ 112

Db 100 VETD-CTTQNTKCRCKSNFF--CNALKCEHCDP 130

QY 113 VALENCASAVADTRCGCKPGWFVEECQVSQC VSSSP 146

Search completed: Tue Jul 25 22:21:15 2000
Job time : 39 secs.

Job time : 39 secs.

 WISE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 25 22:20:00 2000; Maspar time 15.22 Seconds
 871.530 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-314-889-2
 Description: (1-428) from US09314889.pep
 Perfect Score: 3267
 Sequence: 1 MEETQGEAFRGQLRGESAA.....ERMGLDGCVEDLRSLRQGP 428

Scoring table: PAM 150
 GAP 11

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 48.842; Variance 83.135; scale 0.588

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3118	95.4	417	1	WSL1_HUMAN	0.00e+00
2	407	12.5	455	1	TNRI_HUMAN	9.43e-63
3	399	12.2	454	1	TNRI_MOUSE	6.00e-61
4	388	12.2	461	1	TNRI_PIG	1.01e-60
5	383	11.7	461	1	TNRI_RAT	2.35e-57
6	278	8.5	332	1	FASA_PIG	2.14e-34
7	213	6.5	323	1	FASA_BOVIN	5.49e-21
8	211	6.5	324	1	FASA_RAT	1.37e-20
9	204	6.2	327	1	FASA_MOUSE	3.32e-19
10	190	5.8	335	1	FASA_HUMAN	1.77e-16
11	182	5.6	326	1	VT2_MYVL	6.00e-15
12	179	5.5	349	1	VC22_VARV	2.22e-14
13	177	5.4	260	1	CD27_HUMAN	5.28e-14
14	165	5.1	271	1	OX40_RAT	8.94e-12
15	167	5.1	272	1	OX40_MOUSE	3.84e-12
16	168	5.1	461	1	TNRC_HUMAN	2.51e-11
17	164	5.0	325	1	VT2_SPYKA	1.36e-11
18	159	4.9	277	1	CD40_HUMAN	1.10e-10
19	160	4.9	435	1	TNRC_HUMAN	7.29e-11
20	161	4.9	474	1	TNRC_MOUSE	4.80e-11
21	158	4.8	250	1	CD27_MOUSE	1.67e-10
22	157	4.8	415	1	TNRC_MOUSE	2.53e-10
23	153	4.7	656	1	RIP_MOUSE	1.31e-09

24	146	4.5	416	1	NGFR_CHICK	LOW-AFFINITY NERVE GRO	2.24e-08
25	139	4.3	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	3.59e-07
26	134	4.1	671	1	RIP_HUMAN	SERINE/THREONINE PROTE	2.50e-06
27	131	4.0	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	7.88e-06
28	124	3.8	3635	1	LMAS_MOUSE	LAMININ ALPHA-5 CHAIN	1.08e-04
29	116	3.6	799	1	ITB5_HUMAN	INTEGRIN BETA-5 PRECUR	1.96e-03
30	114	3.5	277	1	OX40_HUMAN	OX40L RECEPTOR PRECURS	3.96e-03
31	114	3.5	1247	1	NIDO_HUMAN	NIDOGEN PRECURSOR (ENT	3.96e-03
32	110	3.4	269	1	CD40_BOVIN	CD40L RECEPTOR PRECURS	1.58e-02
33	110	3.4	289	1	CD40_MOUSE	CD40L RECEPTOR PRECURS	1.58e-02
34	111	3.4	655	1	ITB5_PAPCY	INTEGRIN BETA-5 (FRAGM	1.12e-02
35	111	3.4	1607	1	LMG1_MOUSE	LAMININ GAMMA-1 CHAIN	1.12e-02
36	112	3.4	1609	1	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN	7.95e-03
37	108	3.3	103	1	VA53_VACC	PROTEIN A53.	3.12e-02
38	108	3.3	103	1	VA53_VACCV	PROTEIN A53.	3.12e-02
39	109	3.3	400	1	LMB_HTRME	LAMININ B-CHAIN (FRAGM	2.22e-02
40	108	3.3	612	1	OCTC_RAT	PEROXISOMAL CARINITINE	3.12e-02
41	108	3.3	647	1	GAG_SFVL	GAG POLYPROTEIN (CORE	3.12e-02
42	107	3.3	883	1	PGCB_MOUSE	BREVICAN CORE PROTEIN	4.37e-02
43	108	3.3	1245	1	NIDO_MOUSE	NIDOGEN PRECURSOR (ENT	3.12e-02
44	109	3.3	1789	1	LMB1_DROME	LAMININ BETA-1 CHAIN P	2.22e-02
45	109	3.3	3707	1	PGBM_MOUSE	BASEMENT MEMBRANE-SPEC	2.22e-02

ALIGNMENTS

RESULT 1 STANDARD; PRT; 417 AA.
 ID WSL1_HUMAN
 AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
 AC Q99830;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
 DE MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
 DE (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED
 DE RECEPTOR OF DEATH) (LARD).
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
 RC TISSUE=LIMPHOID.
 RX MEDLINE; 97088617.
 RA Kiltson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
 RA Grinham C.J., Brown R., Farrow S.N.;
 RT "A death-domain-containing receptor that mediates apoptosis.";
 RN Nature 384:372-375(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;
 RX MEDLINE; 97081063.
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
 RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
 RT "Signal transduction by DR3, a death domain-containing receptor
 RT related to TNFR-1 and CD95.";
 RN Science 274:990-992(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE; 97148200.
 RA Masters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;
 RT "Apo-3, a new member of the tumor necrosis factor receptor family,
 RT contains a death domain and activates apoptosis and NF-kappa-B.";
 RN Curr. Biol. 6:1669-1676(1996).
 RN [5]
 RP SEQUENCE FROM N.A.

RX	MEDLINE:	G72712273.
RA	RA	Screation G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA	McMichael A.J., Bell J.I.;	
RT	"LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing.";	
RL	Proc. Natl. Acad. Sci. U.S.A.	94:4615-4619(1997).
RN	[6]	
RF	SEQUENCE OF 4-417 FROM N.A.	
RC	TISSUE=BRAIN, AND FETAL LUNG;	
RX	MEDLINE:	97205335.
RA	Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,	
RA	Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,	
RA	Browning J.L., McDonald H.R., Tschoop J.;	
RT	"TRAMP," a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";	
RL	Immunoty 6:79-88(1997).	
RN	[7]	
RP	SEQUENCE OF 7-417 FROM N.A.	
RC	TISSUE=BRAIN;	
RA	Chadhadry P.M., Hood L.E.;	
RA	Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.	
CC	- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B (NF-KAPPAB).	
CC	- DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.	
CC	- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFR1 ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES. APOPTOSIS AND NF-KAPPA B SIGNALING.	
CC	- ALTERNATIVE LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).	
CC	- ALTERNATIVE PRODUCTS: THREE ISOFORMS. WSL-1/LARD-1A (SHOWN HERE), WSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.	
CC	- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.	
CC	- PTM: GLYCOSYLATED (PROBABLE).	
CC	- SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.	
CC	-----	
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CC	or send an email to license@slb.slb.ch .	
CC	-----	
DR	EMBL:	Y093382; CAA70561.1; -
DR	EMBL:	Y093392; CAA70559.1; -
DR	EMBL:	Y093392; CAA70560.1; -
DR	EMBL:	U727633; AAC50819.1; -
DR	EMBL:	U83599; AAB41434.1; -
DR	EMBL:	U83600; AAB41435.1; -
DR	EMBL:	U78029; AAB40918.1; -
DR	EMBL:	U74611; AAB39714.1; -
DR	EMBL:	U94501; AAC51306.1; -
DR	EMBL:	U94504; AAC51309.1; -
DR	EMBL:	U75380; AAC51192.1; -
DR	EMBL:	U75381; AAC51193.1; -
DR	EMBL:	U83597; AAB41432.1; -
DR	HSSP:	P19438; ITNR.
DR	MIM:	603366; -
DR	PFAM:	PF00020; TNFR_c6; 2.
DR	PFAM:	PF00531; death; 1.
DR	PROSITE:	PS00652; TNFR_NGFR_1; 2.
DR	PROSITE:	PS50050; TNFR_NGFR_2; 1.
DR	PROSITE:	PS50017; DEATH_DOMAIN; 1.
KW	Receptor; Apoptosis; Alternative Splicing; Transmembrane; Signal; Repeat.	
FT	CHAIN	1 24 POTENTIAL.
FT	DOMAIN	25 417 WSL-1 PROTEIN.
FT	TRANSMEM	200 220 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	223 417 POTENTIAL.
FT	CYTOPLASTIC	(POTENTIAL).
FT	DOMAIN	334 192 4 X TNFR-CYS.

FT	REPEAT	34	71	TNFR-CYS 1.
FT	REPEAT	72	115	TNFR-CYS 2.
FT	REPEAT	116	163	TNFR-CYS 3.
FT	REPEAT	164	192	TNFR-CYS 4.
FT	DOMAIN	332	413	DEATH DOMAIN.
FT	CARBOHYD	67	67	POTENTIAL.
FT	CARBOHYD	106	106	POTENTIAL.
FT	VARSPLIC	182	218	STLGCSPERCACAVCGMRQFWOYLLAGLVVPLILGA -> VLGGAPGWPCCPPRPMGHPIHLIIPLASAOPGYCR (IN ISOFORM WSL-S1).
FT	VARSPLIC	219	417	MISsing (IN ISOFORM WSL-S1).
FT	VARSPLIC	200	253	MEROVYLGLGVPLLIGTLITLTYYTRHCWPHKPLVTADAEAG MELTLPPEPATHTLS -> SMCWCAKNGRTGDMDGAGEEGC NHPTPSCSGSRSRCSWALMSPSCLdP (IN ISOFORM WSL-S2).
FT	VARSPLIC	254	417	MISsing (IN ISOFORM WSL-S2).
FT	MUTAGEN	354	354	L->A: SUPPRESSES HOMODIMERIZATION, TNFRI INTERACTION, AND APOPTOSIS INDUCTION. L->A: SUPPRESSES HOMODIMERIZATION, AND TNFRI INTERACTION.
FT	MUTAGEN	356	356	D->A: SUPPRESSES HOMODIMERIZATION, AND TNFRI INTERACTION.
FT	MUTAGEN	373	373	RPR -> AAA (IN REF. 6) . RPR -> H (IN REF. 7) . P -> L (IN REF. 6 AND 7) . A -> R (IN REF. 1) . R -> L (IN REF. 1) . R -> H (IN REF. 1) .
FT	CONFLICT	4	6	
FT	CONFLICT	60	60	
FT	CONFLICT	167	167	
FT	CONFLICT	312	312	
FT	CONFLICT	370	370	
FT	CONFLICT	381	381	
SQ	SEQUENCE	417 AA;	45385 MM;	5226319DFDB46706 CRC64;
<hr/>				
Query Match				
Best Local Similarity 95.4%; Score 3118; DB 1; Length 417;				
Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps				
<hr/>				
Db	4	RPRGCCAAVAALLLVLLGARAOGSTSPRODCAGDFHKKIGLFCRCGPAGHYLAAPCTE	63	
Oy	15	RGESAAPVQAALLLVLLGARAOGSTSPRODCAGDFHKKIGLFCRCGPAGHYLAAPCTE	74	
Db	64	PCGNSTCYLCQDPFLFMENHNSECARCOACBEOASVALENCNAVADPRGCKRGMPV	123	
Oy	75	PCGNSTCYLCQDPFLFMENHNSECARCOACBEOASVALENCNAVADPRGCKRGMPV	134	
Db	124	ECOVSOCCVSSEPFYCOPCLDGALHRTRLICSKRHDTDCGTCILPGVEHGDDGCVSCPST	183	
Oy	135	ECOVSOCCVSSEPFYCOPCLDGALHRTRLICSKRHDTDCGTCILPGVEHGDDGCVSCPST	194	
Db	184	LGSCPERCAAVCGMRQFWOYLLAGLVVPLILGATITTYTRHCWPHKPLVTADAEAGMA	243	
Oy	195	LGSCPERCAAVCGMRQFWOYLLAGLVVPLILGATITTYTRHCWPHKPLVTADAEAGMA	254	
Db	244	LTPPATHTLSPIDSAHTLLAPPDSSSEKICVQLVAGNSMTGYPEETOELACPQWTWSMDL	303	
Oy	255	LTPPATHTLSPIDSAHTLLAPPDSSSEKICVQLVAGNSMTGYPEETOELACPQWTWSMDL	314	
Db	304	PSRALGPAAPTLSPESPAGSPAMMLCPGPOLVDVMDAPVARRWKEPVRTLGLIREAIEIA	363	
Oy	315	PSRALGPAAPTLSPESPAGSPAMMLCPGPOLVDVMDAPVARRWKEPVRTLGLIREAIEIA	374	
Db	364	VEVELGRERDOOYEMLTKRMROOPAGIGAYAAALERMGLDGCEVDLRSLORGP	417	
Oy	375	VEVELGRERDOOYEMLTKRMROOPAGIGAYAAALERMGLDGCEVDLRSLORGP	428	
<hr/>				
ID	2	TNRI.HUMAN	STANDARD:	PRT: 455 AA.
AC	P19438:	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TNBP1) (P60) (TNF-R1) (P55) (CD120A).			
OS	Homo sapiens (Human).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE: 90235285.
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V.,
RT "Molecular cloning and expression of a receptor for human tumor
RT necrosis factor.";
RL Cell 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90235284.
RA Loetscher H., Pan Y.-C.E., Lahn H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor.";
RL Cell 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE: 91006021.
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,
RA Aderci D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91090841.
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE: 91017509.
RA Gray P.W., Barrett K., Chantray D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92250049.
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT localization to chromosome 12p13.";
RL Genomics 13:219-224(1992).
RN [7]
RP SEQUENCE OF 41-45.
RX MEDLINE: 90110215.
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT tumor necrosis factor receptor.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX MEDLINE: 93258809.
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE: 97094982.
RA Naismith J.H., Devine T.O., Khono H., Sprang S.R.;

RT	"Structures of the extracellular domain of the type I tumor necrosis factor receptor."
RL	Structure 4:1251-1262(1996).
CC	-I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOTOXICAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.
CC	-I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-I- DOMAIN: THE DOMAIN THAT INDUCES A-SHASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SHASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SHASE.
CC	-I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	-I- DATABASE: NAME=PROM; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".
CC	-----
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CC	-----
DR	EMBL; X55313; CAA39021.1; -
DR	EMBL; M33294; AAA03210.1; -
DR	EMBL; M58286; AAA36753.1; -
DR	EMBL; M63121; AAA36754.1; -
DR	EMBL; M75866; AAA61201.1; -
DR	EMBL; M75864; AAA61201.1; JOINED.
DR	EMBL; M75865; AAA61201.1; JOINED.
DR	EMBL; M60275; AAA36756.1; -
DR	EMBL; A21522; CAA01558.1; -
DR	PIR; A34899; GQHUT1.
DR	PIR; A35010; A35010.
DR	PIR; S12057; S12057.
DR	PIR; A38208; A38208.
DR	PDB; 1TNR; 3I-JUL-94.
DR	PDB; 1NCF; 07-DEC-95.
DR	PDB; 1EXT; 1I-JAN-97.
DR	MIM; 191190; -
DR	PFAM; PF00020; TNFR_c6; 4.
DR	PFAM; PF00531; death; 1.
DR	PROSITE; PS00652; TNFR_NGR_1; 3.
DR	PROSITE; PS00652; TNFR_NGR_2; 3.
DR	PROSITE; PS00652; TNFR_NGR_3; 3.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis; 3D-structure.
KW	3D-structure.
FT	SIGNAL 1 21
FT	CHAIN 22 455
FT	CHAIN 41 291
FT	DOMAIN 22 211
FT	TRANSMEM 212 234
FT	DOMAIN 235 455
FT	DOMAIN 43 196
FT	REPEAT 43 82
FT	REPEAT 83 125
FT	REPEAT 126 166
FT	REPEAT 167 196
FT	DOMAIN 338 348
FT	DOMAIN 356 441
FT	DISELID 44 58
FT	TUMOR NECROSIS FACTOR RECEPTOR 1.
FT	TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	4 X TNFR-CYS.
FT	TNFR-CYS 1.
FT	TNFR-CYS 2.
FT	TNFR-CYS 3.
FT	TNFR-CYS 4.
FT	N-SHASE ACTIVATION DOMAIN (NSD).
FT	DEATH DOMAIN.

FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 FT CARBOHYD 412 412
 FT CONFLICT 443 446
 FT CONFLICT 455 AA; 50494 MM; 4CEPBA96D03B8225 CRC64;
 SQ SEQUENCE

Query Match 12.5%; Score 407; DB 1; Length 455;
 Best Local Similarity 29.9%; Pred. No. 9,43e-63;
 Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDVYCPQSKYTHPNNISICTCKHKGTYLYNDPCPGQDTCRECS 86
 30 ILGARAGGTRSPR-CDCA-GDF-HKRIGLFCGCGPAGHYTLKAPCTEPGNCSTGLVCPQ 86
 Db 87 GSFLASNNHLR-HGLSCSKCKKNGOYEISCTYDROTVCCGRKNQYHHW-SENLFQC- 143
 87 DTFLAMNNHNSCARQACDEQAOVALENGSAVADTRCGCKPWEVECOVSCVSSSP 146
 Db 144 FNSCLGN-GTVH---LSCQEKQNTVC-TCHAGFLEKNCVSCNCKSLCTKLCPL 197
 147 FYCOPCLDCGALHHTRLC-SRDTDCGTCGLPFEYHGDGCVSPTSLG-SCGERC-A 203
 Db 198 QIENVKGTEDSGTVLLP-LVIFFGCLLSLFTGLMTRYGRMWSKLYIVCGSKTPKE 256
 204 AVCGMRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADDA-GME 253
 Db 257 GELGGTTTKPLAHPSPSPGFTPTGFSPPSTFTSSSTYTPGDCPNFAAPREYAP 316
 254 A-LTPPATHTLSPIDS-AHTL-LAPPOSSEKICVQLVGN-WPFGYETQDALCPYT- 308
 Db 317 PYGADPILATALASDPIPNPLQKWEBSAHRPOSJDTDDPALTVAENVPLRKKEFVR 376
 309 -W-SMDQLPSALBPAAAPT-LSP-ESPAQSPAMMLQGPQ-LYDVMADAVAPRRKKEFVR 363
 Db 377 RLGISDHEIDRLQNGCLREAOYSMATRRRRPREATIELLGRVLRMDLGLCED 436
 364 TLGREAIEAVEVEIGR-FRDOQYEMLRKROOP--AGIGAVYALALERMGLDGCVED 419
 Db 437 IEEL 441
 QY 420 LRSRL 424

RESULT 3
 ID TNR1 MOUSE STANDARD; PRT; 454 AA.

AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNRSF1A OR TNR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91187885.
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species

RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91246168.
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91285014.
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Rissonerghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN.
 RX MEDLINE; 92039815.
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94245292.
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";
 RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93156721.
 RA Rothe J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175(1993).
 CC -I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CAULED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
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 CC
 DR EMBL; M60468; AAA39751.1; -
 DR EMBL; M59377; AAA40464.1; -
 DR EMBL; X59238; CAA41922.1; -
 DR EMBL; X57796; CAA40936.1; -
 DR EMBL; L26349; AAA59361.1; -
 DR EMBL; M76656; AAA40465.1; -
 DR EMBL; M88067; AAA40465.1; JOINED.
 DR EMBL; M76655; AAA40465.1; JOINED.
 DR PIR; A38634; GOM511.

	FT	DISULFID	168	179	BY SIMILARITY.
FT	DISULFID	182	190	BY SIMILARITY.	
FT	DISULFID	185	194	BY SIMILARITY.	
FT	CARBOHYD	54	54	POTENTIAL.	
FT	CARBOHYD	86	86	POTENTIAL.	
FT	CARBOHYD	145	145	POTENTIAL.	
FT	CARBOHYD	151	151	POTENTIAL.	
SC	SEQUENCE	461 AA;	50696 MM;	CD72361EC60C9D43 CRC64;	
Query Match		12.2%;	Score 398;	DB 1:	Length 461;
Best Local Similarity		32.3%;	Pred. No. 1,01e-60;		
Matches 139;	Conservative	81;	Mismatches 160;	Indels 51;	Gaps 32.
Db	33	HPGDEKRESLCPOQKYSHPQNRISICCTCKHGTUHLNDCIGPLDIDRCEDNGFTTAS	92		
Qy	36	OGGTRSPR-CCDA-GDF-HKKIGLGGCGAGNHILAPCEPQGNSTCLVCPQDPLAW	92.		
Db	93	ENHL-TOGLSCSKCRSEMSQVIEISCTYVDRTDYGCKRN--QYR-KY-WSETLF-Q-C	143		
Qy	93	ENHNSECARCOACEASQVALEKSCSAVADTRGCKRGWFEQVQSQVSSPFCOPC	152		
Db	144	LNC-SLCNGVYOLPCLKEOPTON-CHSGPEFLDKKEVSCVGNKNMCKMLCPATSETR	201		
Qy	153	LDCGLAHRH-T-RLIC-SRDTDGTCLPBGVEHGDGCVPTSLDSCPERCAVCGWR	209		
Db	202	NDFOGTGTVLLPLVIFPGCLAEFLFGLACRYOR-WKPLYSIIGKSTPYKEGEP	260		
Qy	210	QMFV--VOVILLA-----GLVPLPLGATLTYTRHCPHK--PLV-----TA-DEAGMEA	254		
Db	261	IATASFQPIITFSPIPSFTTSSPVPSPSPISPTFTCDMSNIKVPSPKEIAPP	320		
Qy	255	I-TTP--PAHLSPDLS-AHTL-LAPDSSERKCTVOLGNSMP--GIPTQALCP	305		
Db	321	OGAGILMPAPSTVPTPLPKMGSSAHSAPAOIADADPATLYAVVDGVPTRNKEF	380		
Qy	306	QVTWMDQLP-SRALGPAAPTL--SPESPAGSPAMLQPGPO-LYVDMAVAPARMKF	361		
Db	381	VARGLSEHETRLQLONGRCLEKREQYISMLAEKRRKTRRRATELEGLSVLRDDILGCL	440		
Qy	362	VTDLIRLEALELVAEVEIGR-FRDOQYEMLRKMOO-QP-AGLGAVYAALERMGLOGCV	417		
Db	441	EDIEEAL-RGP	450		
Qy	418	EDLRSRLQRP	428		
RESULT	5				
ID	TNRI-RAT	STANDARD:	PRT:	461 AA.	
AC	P22934:				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-MAR-1992 (Rel. 21, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).				
GN	TNFRSF10R OR TNFR1 OR TNFR-1.				
OC	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 91090841.				
RA	Himmler A., Maurer-Pogy I., Kroenke M., Scheurich P., Pfizenmaier K.,				
RA	Lantier M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;				
RT	Molecular cloning and expression of human and rat tumor necrosis				
RT	factor receptor chain (p60) and its soluble derivative, tumor				
RT	necrosis factor-binding protein.";				
RL	DNA Cell Biol. 9:705-715(1990).				
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD				
CC	RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING				
CC	AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)				
CC	PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE				
CC	SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE				
CC	PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).				
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO				

	CC	HOMORIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
	CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
	CC	-I- SIMILARITY: CONTAINS A LA-NRPR/TNRF-TYPE CYSTEINE-RICH REGION.
	CC	-----
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
	CC	-----
DQ	EMBL; M63122; AAA42256.1; -	
DR	PIR; B36555; B36555.	
DR	HSSP; P19438; TNR.	
DR	Pfam; PF000020; TNFR_C6; 4.	
DR	Pfam; PF005031; death; 1.	
DR	ProSITE; PS00652; TNFR_NGRF_1; 3.	
DR	ProSITE; PS50050; TNFR_NGRF_2; 3.	
DR	ProSITE; PS50017; DEATH_DOMAIN; 1.	
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis. SIGNAL	
FT	SIGNAL	1..21
FT	CHAIN	22..461
FT	TDOMAIN	22..211
FT	TRASMEM	212..234
FT	TDOMAIN	235..461
FT	TDOMAIN	43..196
FT	REPEAT	82..82
FT	REPEAT	83..125
FT	REPEAT	126..166
FT	REPEAT	167..196
FT	DOMAIN	344..354
FT	DOMAIN	363..448
FT	DISULFD	44..58
FT	DISULFD	59..72
FT	DISULFD	62..81
FT	DISULFD	84..99
FT	DISULFD	102..117
FT	DISULFD	105..125
FT	DISULFD	127..143
FT	DISULFD	146..158
FT	DISULFD	149..166
FT	DISULFD	168..179
FT	DISULFD	182..191
FT	DISULFD	185..195
FT	CARBOHYD	54..54
FT	CARBOHYD	151..151
FT	CARBOHYD	201..201
SQ	SEQUENCE	461 AA; 50969 MW; EB23C05450FBBD202 CRC64;
	Query Match	11.7%; Score 383; DB 1; Length 461;
	Best Local Similarity	29.8%; Pred No. 2,35e-57;
	Matches 125; Conservative	73; Mismatches 165; Indels 37; Gaps 31.
DQ	35 GDEKRDNLCPGGKYAHPRKNNSICCTKCHKGTGYIVSDCPSPGETVCEYCDKGTTASQN	94
	I :	
OY	38 GFPSRPCD-CA-GDF-HKKIGLCFCRCGPCAGHYTLAKPTEPCGNSTCLVCYPQDTFLMEN	94
DQ	95 H-VROGLSKTKRKMEKFQEYSPPCADMDTYCGCKKNGFOXYRLSETHPGCVDSPCFNGT	153
	: :	
OY	95 HNHSFCARQCADBEAQSVALENCACVAADVTRGCGRGFVFEC--QVS-QCYSSSP-FYCQ	150
DQ	154 VTIPCKE-KONTVVONCHAGFEFLSGNECPSCSHCKKNOCMKLICLPYANVTNPDSGTAV	212
	: :	
OY	151 PCLDGALARRHRIILCSRDDTCG-LCP-GRYEHDGCVS-C-PYSLTGSCPCCAAYC	206
DQ	213 LLEPLVFGDLCLLFICSLLCRCYQMHPRYVISITCRSAAPVKVEEGEITRTKLTPASI	272

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OY 207 GWRQMFVGV-LLAGLVPL--LGATLTYYRH-CMPKPLVADACG--EALTPPPA 260
DB 273 PAFSPRPGNPTLGFSTTRFRSHVSTPISPFGPSNMHNFPVPPREVPTQ-G-A-DP 329
OY 261 THLSPDLS-AHTL-LAP-DDSSEKICTYQL--V-GNS-WTPGYPEQALCPQVTSWDQ 313
DB 330 LLTGSINPVIPAPVKKMEDVAAOPORLDTADPMLYAVDGVPTRMKEFRLLGLSE 389
OY 314 LPSRALGPPAAAT-LSP-ESPAGSPMMQLPG-PQ-LYDVMDVAPARMKEFRTGLRE 369
DB 390 HEIERLEGRCLREAHYSMLEAMRRRTPRHEATLDVYGRVLCMDMLNGLCLENIRETLE 449
OY 370 AELEAVEVEIGR-FRDQYEMLRKMRQOP--AGLGAVYALERGLDGCVEDLRSRLQ 425

RESULT 6
ID FASA_PIG STANDARD: PRT: 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DB EMBL: AJ001203; CA04596.1; -
DR PFAM: PF000020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 332 FASL RECEPTOR.
FT DOMAIN 17 175 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 176 192 POTENTIAL.
FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 164 3 X TNFR-CYS.
FT REPEAT 45 81 TNFR-CYS 1.
FT REPEAT 82 125 TNFR-CYS 2.
FT REPEAT 126 164 TNFR-CYS 3.
FT DOMAIN 227 311 DEATH DOMAIN.

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FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 116 116 POTENTIAL.
SQ SEQUENCE 332 AA; 37592 MM; 5B8B03662756BFB1B CRC64;

Query Match 8.5%; Score 278; DB 1; Length 332;
Best Local Similarity 38.2%; Pred. No. 2,14e-34;
Matches 42; Conservative 21; Mismatches 38; Indels 9; Gaps 7;

DB 45 ECPFGQHRE-GQFCPCPCPCPKRRKADCTSPGAPQCPGCEGEYTD-KNHSSKCRRC 102
OY 45 DCAADFHKIKIGLFCPCRCRCPAGHYLKAPCTEPCGNSCTLCYPO-DTFLAMENHNSECARC 103
DB 103 RVCGEGHLEVE-KNCTRTONTKCRCKRNP--CHTSCCHCNP--CTTC 147
OY 104 QACD-EQASQVALLNCNSAVADTRCGCKRGWTEGVQSVSSPPYCPQC 152

RESULT 7
ID FASA_BOVIN STANDARD: PRT: 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 96226401.
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DB EMBL: U34794; AAC48546.1; -
DR HSP: P25445; IDDF.
DR PFAM: PF00020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 FASL RECEPTOR.
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 188 POTENTIAL.
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 163 3 X TNFR-CYS.
FT REPEAT 45 80 TNFR-CYS 1.

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FT	REPEAT	81	124	TNFR-CYS 2.
FT	REPEAT	125	163	TNFR-CYS 3.
FT	DOMAIN	238	306	DEATH DOMAIN.
SO	SEQUENCE	323 AA;	36445 MM;	4D8BA90E9E1F4892 CRC64;
Query Match				
	Best Local Similarity	29.5%;	Score 213;	DB 1; Length 323;
	Matches	31; Conservative	24; Mismatches	43; Indels 7; Gaps 5;
Db	55	FCGCPPEPKRRNGDCKRQDTPRECVLCSEGENEYTD-KSHSDKCIKRCISIDEEHGLEVE	113	
Oy	57	FCRCRCRPGHLYKACPTCEPCGNCSTLCVCPQ-DTEFLAMENHNHSECARCQACDEQASQVAL	115	
Db	114	ONCSTRTNTRKCKRCKSNF--CNSSPCHEONP--CTTC-ENGIIIEK	153	
Oy	116	ENGSNAVDRCCGKFGWFEYECQVSSQCVSSSPYCCPCIDCGALHR	160	
RESULT	8	STANDARD:	PRT;	324 AA.
ID	FASL_RAT			
AC	063199;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)			
DE	(APO-1 ANTIGEN) (CD95).			
GN	Ap1 or FAS.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;			
RX	MEDLINE: 94128114.			
RA	Kimura K., Yamamoto M., Wakatsuki T.;			
RT	"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver."			
RL	Biochem. Biophys. Res. Commun. 198;666-674(1994).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED SUCIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	-----			
DR	EMBL: D26112; BAA05108.1; -			
DR	PFAM: PF00020; TNFR.c6; 3.			
DR	PFAM: PF00531; death; 1.			
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE: PS50050; TNFR_NGFR_2; 1.			
DR	PROSITE: PS50017; DEATH_DOMAIN; 1.			
KW	Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.			
FT	SIGNAL	1	21	BY SIMILARITY.
FT	CHAIN	22	324	FASL RECEPTOR.
FT	DOMAIN	22	171	INTRACELLULAR (POTENTIAL).
FT	TRANSMEM	172	188	POTENTIAL.
FT	DOMAIN	189	324	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	43	163	3 X TNFR-CYS.

FT	REPEAT	43	79	TNFR-CYS 1.
FT	REPEAT	80	123	TNFR-CYS 2.
FT	REPEAT	124	163	TNFR-CYS 3.
FT	DOMAIN	219	303	DEATH DOMAIN.
FT	CARBOHYD	43	43	POTENTIAL.
FT	CARBOHYD	114	114	POTENTIAL.
FT	CARBOHYD	132	132	POTENTIAL.
SO	SEQUENCE	324 AA;	36835 MM;	D25D583C909D9D09 CRC64;
Query Match 6.5%; Score 211; DB 1; Length 324;				
Best Local Similarity 30.1%; Pred. No. 1,3/e-20;				
Matches 37; Conservative 26; Mismatches 47; Indels 13; Gaps				
Db	43 NCSESLYO-VPEFCCOPCPQPERKVKD-CITSGGAPCPCHPCTEGEEYTDK-KHYSDCRR 99			
OY	45 DCAGGFHKIKILFCRCRGPAC-HYLMKAPCTBPCGNSCTCLVQP-QDTFLAMENHNNSCAR 102			
Db	100 CAFCDGEGHLEVE-TNCTRTONTCKRCENFY--CNMSLC-DHC-YHCTSCGLE-DLLEP 155			
OY	103 COACGE-QASQVALENCSAVADVTRGCKPFWFVECOVSQCVSSSPFYCQPC-IDCGALHR 160			
Db	154 CTR 156			
OY	161 HTR 163			
RESULT	9			
ID	FASA_MOUSE	STANDARD;	PRF;	327 AA.
AC	P25446;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)			
DE	(APO-1 ANTIGEN) (CD95).			
GN	API1 OR FAS.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 92148151.			
RA	Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,			
RT	Copeland N.G., Jenkins N.A., Nagata S.;			
RT	"The cDNA structure, expression, and chromosomal assignment of the			
RT	mouse Fas antigen."			
RL	J. Immunol. 148:1274-1279(1992).			
RN	[2]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE: 93189576.			
RA	Adachi M., Watanabe-Fukunaga R., Nagata S.;			
RT	"Aberrant transcription caused by the insertion of an early			
RT	transposable element in an intron of the Fas antigen gene of 1pr			
RT	mouse."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).			
RN	[3]			
RP	VARIANT LPR.			
RX	MEDLINE: 92195401.			
RA	Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Nagata S.;			
RT	"Lymphoproliferation disorder in mice explained by defects in Fas			
RT	antigen that mediates apoptosis."			
RL	Nature 356:314-317(1992).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE			
CC	ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE DEATH-INDUCING			
CC	RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING			
CC	SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC			
CC	ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF			
CC	CASPASES (ASPARTATE-SPECIFIC CYSSTEINE PROTEASES) MEDIATING			
CC	APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE			
CC	INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED			
CC	SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS			
CC	-1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS			

Query Match 5.8%; Score 190; DB 1; Length 335;


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RM [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MONOCYTES:
RX MEDLINE: 92013149.
RA Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
RT "The T cell activation antigen CD27 is a member of the nerve growth
RL factor/tumor necrosis factor receptor gene family.";
RN J. Immunol. 147:3165-3169(1991).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93094588.
RA Loenen W.A., Gravestien L.A., Beumer S., Melief C.J., Hagemeijer A.,
RT Borst J.;
RT "Genomic organization and chromosomal localization of the human CD27
gene.";
RL J. Immunol. 149:3937-3943(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
CC A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.
CC -1- PTM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD27 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL: M63928; AAA58411.1; -.
DR PIR: A46454; A46454.
DR PIR: A46517; A46517.
DR HSSP: P19438; INCF.
DR MIM: 186711; -.
DR PFAM: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00650; TNFR_NGFR_2; 1.
DR T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 1 260 CD27L RECEPTOR.
FT DOMAIN 21 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 212 POTENTIAL.
FT DOMAIN 213 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 141 3 X TNFR-CYS.
FT REPEAT 26 63 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 POTENTIAL.
FT MOD RES 219 219 PHOSPHORYLATION (POTENTIAL).
FT COMPLOC 59 59 A -> T (TN REF. 2)
SQ SEQUENCE 260 AA: 29156 MW: 43038922FA90DE2 CRC64:
Query Match 5.4%; Score 177; DB 1; Length 260;
Best Local Similarity 25.2%; Pred. No. 5.28e-14;
Matches 32; Conservative 36; Mismatches 50; Indels 9; Gaps 7;
Db 4 PRRMVLGVIGTIVGTSATAPK-SCPERHYMAQKICCCMCRCGTFLVKCDQHRRAQC 62
OY 23 PQALLLVLLGA-RAOGGTRSPRCDCAGDFHKKIGLFCCKCPAGHYLKAPCTPCGNGSTC 81
Db 63 DPCIGVSPSP-DHHTRPSCSRHCN--SGLL-VNCCITTAACACRGM--QCRDKE 116
OY 82 LVC-PQDTFLAMENHNHNSCARCQACDQASQVALENCASVADTRCGCKGKGMVECVSQ 140
Db 117 CTECDPL 123
OY 141 CVSSSPF 147

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RESULT 14
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MNC OX40).
GN TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-T-CELL;
RX MEDLINE: 90214614.
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL lymphocytes -- a molecule related to nerve growth factor receptor.";
CC EMBL J. 9:1063-1068(1990).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
-----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL: X17037; CAA34897.1; -.
DR PIR: S08036; S08036.
DR PIR: S12783; S12783.
DR HSSP: P25942; ICDF.
DR PFAM: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 1 20 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 POTENTIAL.
SQ SEQUENCE 271 AA: 29895 MW: C06465136B1E821 CRC64:
Query Match 5.1%; Score 165; DB 1; Length 271;
Best Local Similarity 29.7%; Pred. No. 8.94e-12;
Matches 22; Conservative 17; Mismatches 32; Indels 3; Gaps 3;
Db 37 CCRGCPGHCWVSHC-DHTRDTVCPC-EPGPN-EAVNYDPCKQCTCNHRSSELKON 93
OY 58 CCRGCPAGHYTKAPCTPCGNGSTCLVCPQDTFLAMENHNHNSCARCQACDQASQVALEN 117
Db 94 CTPEDTVQCQCRPG 107
OY 118 CSAVADTRCGCKPG 131
RESULT 15
ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)

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OC Eumariota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
OC Mammalia: Eutheria: Primates: Catarrhini: Hominae: Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE: 90235285.
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.,
RT "Molecular cloning and expression of a receptor for human tumor
RL Cell 61:361-370(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90235284.
RA Loetscher H., Pan Y.-C.E., Lahn H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.,
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor."
RL Cell 61:351-359(1990).
[3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE: 91006021.
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,
RA Aderka D., Holtmann H., Wallach D.,
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor."
RL EMBO J. 9:3269-3278(1990).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91090841.
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Haubmann R., Stratowa C., Adolf G.R.,
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein."
RL DNA Cell Biol. 9:705-715(1990).
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE: 91017509.
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.,
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein."
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92250049.
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.,
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RL localization to chromosome 12p13.".
RN Genomics 13:219-224(1992).
[7]
RP SEQUENCE OF 41-45.
RX MEDLINE: 90110215.
RA Engelmann H., Novick D., Wallach D.,
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors."
RL J. Biol. Chem. 265:151-1536(1990).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX MEDLINE: 93258809.
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.,
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.".
RL Cell 73:431-445(1993).
[9]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE: 97094982.
RA Natsmith J.H., Devine T.O., Khono H., Sprang S.R.,

RT	"Structures of the extracellular domain of the type I tumor necrosis factor receptor."
RL	Structure 4:1251-1262(1996).
CC	-I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR, THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOSOLIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.
CC	-I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-I- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC	-I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	-I- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm"
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outpost on the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, X55313; CAA39021.1; -;
DR	EMBL, M33294; AAA03210.1; -;
DR	EMBL, M58286; AAA36754.1; -;
DR	EMBL, M63121; AAA36754.1; -;
DR	EMBL, M75866; AAA61201.1; -;
DR	EMBL, M75864; AAA61201.1; JOINED.
DR	EMBL, M75865; AAA61201.1; JOINED.
DR	EMBL, M60275; AAA36756.1; -;
DR	EMBL, A21522; CAA01558.1; -;
DR	PIR, A34899; GQHUT1.
DR	PIR, A35010; A35010.
DR	PIR, S12057; S12057.
DR	PIR, A38208; A38208.
DR	PDB, 1TNR; 3I-JUL-94.
DR	PDB, INCF; 07-DEC-95.
DR	PDB, TEXT; 11-JAN-97.
DR	MIM: 191190; -;
DR	PFAM; PF00020; TNFR_c6; 4.
DR	PFAM; PF00531; death; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis; 3d-structure.
FT	SIGNAL 1 21
FT	CHAIN 22 455
FT	CHAIN 41 291
FT	DOMAIN 22 211
FT	TRANSMEM 212 234
FT	DOMAIN 235 435
FT	DOMAIN 43 196
FT	REPEAT 43 82
FT	REPEAT 83 125
FT	REPEAT 126 166
FT	REPEAT 167 196
FT	DOMAIN 338 348
FT	DOMAIN 356 441
FT	DISEUID 44 58
CC	TUMOR NECROSIS FACTOR RECEPTOR 1.
CC	TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
CC	EXTRACELLULAR (POTENTIAL).
CC	POTENTIAL.
CC	CYTOPLASMIC (POTENTIAL).
CC	4 X TNFR-CYS.
CC	TNFR-CYS 1.
CC	TNFR-CYS 2.
CC	TNFR-CYS 3.
CC	TNFR-CYS 4.
CC	N-SMASE ACTIVATION DOMAIN (NSD).
CC	DEATH DOMAIN.

DR PIR: S16677; S16677.
 DR PIR: S19021; S19021.
 DR HSSP: P19438; 1EXT.
 DR MGD: MGI-1314884; TNFRSF1A.
 DR PFAM: PF00020; TNFR_c6; 4.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00500; TNFR_NGFR_2; 3.
 DR PROSITE: PS0017; DEATH_DOMAIN; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT DOMAIN 22 212 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT TRANSMEM 213 235 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 236 454 POTENTIAL.
 FT DOMAIN 43 196 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 43 82 4 X TNFR-CYS.
 FT REPEAT 83 125 TNFR-CYS 1.
 FT REPEAT 126 166 TNFR-CYS 2.
 FT REPEAT 167 196 TNFR-CYS 3.
 FT REPEAT 196 349 TNFR-CYS 4.
 FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 356 441 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 191 BY SIMILARITY.
 FT DISULFID 185 195 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 202 202 POTENTIAL.
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SO SEQUENCE 454 AA; 50129 MW; 0710C2E8C3286D9 CRC64;

Query Match 12.5%; Score 399; DB 1; Length 454;
 Best Local Similarity 28.7%; Pred. No. 1,49e-60;
 Matches 119; Conservative 79; Mismatches 182; Indels 34; Gaps 28;

DB 40 RDSLCP-OGKYVHSKNNISCTCKHKGTYLVSDCPSPGDTVCRCCEKCTFTASQMYLR- 97
 QY 29 RSPRCDCAQDF-HKKIGLFCRCGCGAGHLLKAPCTEPCGNSYCLVCPQDTFLAMENHNS 87
 DB 98 QLSCKTCKREMSQVEISFCQADKDTVCCKENOFQRYLSETHFOCVDCSPCFNGTVTIP 157
 QY 88 ECARQACDEQASQVALEMSAVADTRCGCKRGWVEEC--QVS-QCVSSSP-FYQCPCLD 143
 DB 158 CKETO-NIVCNCHAGFELRESCVPC--SHCKKNECKMLCLPPPLANTYNTPODSTAVL 214
 QY 144 CGALHRRHRLIC-SR---RDTGCGTCLPGFYEHGDCVVS-CPTSTIGSC--PERCAAVCG 196
 DB 215 LPLVLLIGLCLISFIFISIMCMRYPRMRREVYSILICRDPV-KKEEAKG-PLTPASPAF 272
 QY 197 WRQMWVQV-LLAGLVVPL-LGATL-TYTRYH-CWPHKPLVTADAGMEALTPPATHL 252
 DB 273 SPTSGFNPLTGFSTGFSSPVSTP-ISPIFGPSNMHFMPPVSEVVPOTGADPLLTESIC 331
 QY 253 SPLDS-AHTL-LAPDSSSKICTVQLVGSMTFPGYETQALCPQV-TWSMQLPBRALG 309
 DB 332 SVPAFTSVQKEDSAHPQRPADLAILEYAVDVGPAPAKEMFMRMGISEHIEIRLEMQ 391
 QY 310 PAAPATLPSPPAGS-PAMMLQPG-POLYDVMDAVPARMKFEVFTLIGRAEIEAVEVE 367
 DB 392 NGRCLEAOYSLEAMBRRTPRHEDTLEVYGLVSKMNLAGELENTLEAL-RNP 444
 QY 368 IGR-FRDOOYEMLKRMOQP--AG-LGAVYALERMGIDGCEVEDLRSLRQGP 417

RESULT 4
 ID TNRL_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P50) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE; 9601645.
 RA Suter B., Paul U.H.;
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
 receptor.";
 RL Gene 163:263-266(1995).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE
 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U19994; AAC48499.1; -.
 DR HSSP: P19438; 1TNR.
 DR PFAM: PF00020; TNFR_c6; 3.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00500; TNFR_NGFR_2; 2.
 DR PROSITE: PS0017; DEATH_DOMAIN; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 22 210 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT TRANSMEM 211 233 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 234 461 POTENTIAL.
 FT DOMAIN 43 195 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 43 82 4 X TNFR-CYS.
 FT REPEAT 83 125 TNFR-CYS 1.
 FT REPEAT 126 166 TNFR-CYS 2.
 FT REPEAT 167 195 TNFR-CYS 3.
 FT REPEAT 195 350 TNFR-CYS 4.
 FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 362 447 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 190 BY SIMILARITY.
 FT DISULFID 185 194 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 145 145 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 SQ SEQUENCE 461 AA; 50969 MW; CD72361EC60C9D43 CRC64;

Query Match 12.4%; Score 398; DB 1; Length 461;
 Best Local Similarity 32.3%; Pred. No. 2.50e-60;
 Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

DB 33 HPGRKRESICPOGKYSHPNRSICCTKHKGTLYVLSVDSGPGQETVCEVCKGTFTAS 92
 25 QGGRSRPR-CCCA-GDF-HKKIGLFCGCGPAGHYLKAFCPEGNSNCLVOPDPTFLAW 81
 -DB 93 ENHL-TQCLSCSKCRSEMSQVEISPTVDRDVTGCGKRN--QYR-KY-MSYLE-Q-C 143
 82 ENHNSSECARQACDEQASQVLALENCASVADTRCGCKPGMEVEQVSOVSSSPYCOPC 141
 DB 144 LNC-SLCPNGVQVPLEKOPTICN-CHSGFPLRKEGVSCVNCNADCKNCPATSETR 201
 142 LDCGALHRH-T-RLIC-SRDPDGTCLPGFYEHEGDCVSCPTSLGSCPEKCAVCGMR 198
 DB 202 NDFDGTGTVLLPIVIFGLCLAFELFVGLACRYOR-WKPKLYSLICKSKPTVKEGDEP 260
 199 QMFV---VOVLLA-----GLVVPILLGATLYTYRHCKPHEK-PLV-----TA-DEAGMEA 243
 QY 261 LAIAPSPGPTTSPSPSPPTTSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 320
 244 L-TTP---PATHLSPDLS-AHTL-LAPDSSSEKICTVOLVGNMTP---GYPETOEALCP 294
 DB 321 OGACPIILPMRPAHPVPLPKWGSASHASAPQALADADATATLYAVDVGPPRWKEF 380
 295 QVTWSMDLP-SRLDGPAAATL--SPESPAGSPAMMLQPGQ-LYDWDADAPARRKEF 350
 QY 381 VRRGLSHEIERLELONGRCLEAREAYSMLEWRRTSRREATELLLSGLNDMLGCL 440
 351 VRTGLRAELEAVEVEIGR-FRQGYEMLRKWRQ--QP-AGLQAVYAALERMGLDGV 406
 DB 441 EDIEBAL-RGP 450
 QY 407 EDLRSRLQGRP 417

RESULT 5
 ID TNRI-RAT STANDARD; PRT; 461 AA.
 AC P22934;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91090841.
 RA Hammar A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein.";
 RL DNA Cell Biol. 9:705-715(1990).
 CC FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M63122; AAA42256.1; -;
 CC PIR; B36555; B36555.
 CC HSSP; P19438; 1TNF.
 CC PFAM; PF00020; TNFR_C6; 4.
 CC PFAM; PF00531; death_1; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00650; TNFR_NGFR_2; 3.
 CC PROSITE; PS0017; DEATH_DOMAIN; 1.
 CC Receptor; Transmembrane; Glycoprotein; Repeat; signal; Apoptosis.
 CC CHAIN 1 21
 CC SIGNAL 1 21
 CC DOMAIN 22 461
 CC TRANSMEM 212 234
 CC DOMAIN 235 461
 CC DOMAIN 43 196
 CC DOMAIN 43 196
 CC REPEAT 83 125
 CC REPEAT 126 166
 CC REPEAT 167 196
 CC REPEAT 363 448
 CC DOMAIN 344 354
 CC DOMAIN 353 448
 CC DISULFID 44 58
 CC DISULFID 59 72
 CC DISULFID 62 81
 CC DISULFID 84 99
 CC DISULFID 102 117
 CC DISULFID 105 125
 CC DISULFID 127 143
 CC DISULFID 146 158
 CC DISULFID 149 166
 CC DISULFID 168 179
 CC DISULFID 182 191
 CC DISULFID 185 195
 CC CARBOHYD 54 54
 CC CARBOHYD 151 151
 CC CARBOHYD 201 201
 CC SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

Query Match 12.0%; Score 383; DB 1; Length 461;
 Best Local Similarity 29.8%; Pred. No. 5.52e-57;
 Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;

DB 35 GDEKRDNLCPQKGYAHPRNNSICTCKHKGTLYVLSVDSGPGQETVCEVCKGTFTAS 94
 27 GRSRPRCD-CA-GDF-HKKIGLFCGCGPAGHYLKAFCPEGNSNCLVOPDPTFLAW 83
 QY 95 H-VROGLSCKTCKEMFQVEISPTCKRADMOTVCGCKRNQGRYLSHPCQVDCSPFNGT 153
 DB 84 HNSSECARQACDEQASQVLALENCASVADTRCGCKPGMEVEE--QVS-QCVSSP-fyCQ 139
 QY 154 VTIPIKE-KONTVNCNHAQFPLSGNECTPCSHCKNCKEOMKCLPVAVNTNPDSGTAV 212
 DB 140 PCIDCGALHRHRLICSRDPTDGT-CLP-GFYEHEGDCV-C-PLSTIGSCPEKCAVCG 195
 QY 213 LPLVIFGLCLLFFICISILCRYPQWRPVYSIICRDSAPYKEVGEIGVTKPLTPASI 272

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OY 196 GMRQMWVQV-LLAGLVPL--LGATLVYTH-CMPHKPLVADAGM--EALTPPPA 249
DB 273 PAFSPNPGNPLIGSTTPFHSVSTPISPVFGSPNHNINPVYREVPYTO-G-A-DP 329
OY 250 THLSPLDS-AHTL-LAP-PPSSSEKICTVOL-V-GNS-WTPGYETQELCPQWTWMDQ 302
DB 330 LLYGSLNPVPIPAVRKMEVYVAAQPORLDTADPAMLXAVVDGVPYTRKMEFMTLGLSE 389
OY 303 LBSRALGPAAPT-LSP-ESPAGSPAMLOPG-PQ-LYDMDAVPARMEFVTLGLRE 358
DB 390 HEIERELANGRCLEAHVSMLEAMRKTRPRHEATLDVYGRVLCDDMLRCLENIREFLE 449
OY 359 AELEAVEVEIGR-FRDQGYMLKRMHQGP---AGLCAVVAALERMGLDQVEDLRSRLQ 414

RESULT 6
ID FASA_PIG STANDARD; PRT; 332 AA.
AC 07736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Sus. scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 116 116 POTENTIAL.
SQ SEQUENCE 332 AA; 37592 MW; 588B03682756BFLB CRC64;

Query Match
Best Local Similarity 38.2%; Pred. No. 3.52e-34;
Matches 42; Conservative 21; Mismatches 38; Indels 9; Gaps 7;

DB 45 ECPGQHNE-GQPCQPPKPKRRKADCTSPGAGQCYPCSGEGEYTD-KNHSSKCRRC 102
OY 34 DCAADFHKRIQLFCCRCRGPAGHYLKAPCTEPGNTCLVCPD-DYFLWMENHNSEGCARC 92
DB 103 RVCCGHELEVE-KNCTRTONTKRCRKNPF--CCTSCECHNP--CTTC 147
OY 93 QACD-EQASQVALENCASVADTRCGCKRGWYECOVSSCPYCCPC 141

RESULT 7
ID FASA_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine fas."
RL DNA Cell Biol. 15:227-234(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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or send an email to license@sib-sib.ch).
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FT REPEAT      81    124      TNFR-CYS 2.
FT REPEAT      125   163      TNFR-CYS 3.
FT DOMAIN      238   306      DEATH DOMAIN.
SQ SEQUENCE     323 AA; 36445 MW; 4D88A90E9E1EF4892 CRC64;

Query Match      6.7%; Score 213; DB 1; Length 323;
Best Local Similarity 29.5%; Pred. No. 7,37e-21;
Matches 31; Conservative 24; Mismatches 43; Indels 7; Gaps 5;

Db      55 FCCQCPGPKRRKNGDKRKRDGDTPEVCLCSEGNEXTD-KSHSHDCKIRCSDIEEHGLEVE 113
Oy      46 FCCRCRCAGHYLAKAPCTGPCGNSITCLVQD-DTEFLAMENHHNSCARCAQACDEQASVAL 104
Db      114 ONCTRTNTKCRCKSNF--CNSSPCEHCNP--CTTC-EHIIIRK 153
Oy      105 ENCSAVADTRCGCKPGWEFCOVSSCVSSPFYCPCLDGCALHR 149

RESULT      8
AC FASA_RAT STANDARD: PRI: 324 AA.
AC Q63199;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE; 94128114.
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
RT the rat liver";
RL Biochem. Biophys. Res. Commun. 199;666-674(1994).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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DR EMBL: D26112; BAA05108.1; -.
DR PFAM: PF00020; TNFR_c6; 3.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
DR PROSITE: PS50050; TNFR_NGFR_3; 2.
DR PROSITE: PS50017; DEATH DOMAIN; 1.
KM Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 324 FAST RECEPTOR.
FT DOMAIN 22 171 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 172 188 POTENTIAL.
FT DOMAIN 189 324 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 163 3 X TNFR-CYS.

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FT REPEAT 43 1/3 TNR-CYS 1.
FT REPEAT 80 123 TNR-CYS 2.
FT REPEAT 124 163 TNR-CYS 3.
FT DOMAIN 219 303 DEATH DOMAIN.
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 114 114 POTENTIAL.
FT CARBOHYD 132 132 POTENTIAL.
SQ SEQUENCE 324 AA: 36835 MW: D25D583C909D9D09 CRC64;

Query Match 6.6%; Score 211; DB 1; Length 324;
Best Local Similarity 30.1%; Pred. No. 1,836-20;
Matches 37; Conservative 26; Mismatches 47; Indels 13; Gaps 1

Db 43 NCSEBGLY-VGPFCOPCOPGERKYVD-CTTSGAPATCPHCTGEGEYTR-KHYDKCR 99
Oy 34 DCADGFHKIKGLFCCRCRCPRAG-HYIKAPCTPCGNSCTLCVCPQ-DTFIWMENHHNSCAR 91
Db 100 CAFCDGEGHLEVE-TNCTPIONTKCKCKENFY--CNASLC-DHC-YHCISGLE-DLEP 153
Oy 92 COACDE-QASQVALENCSSAVADTRCGCKPGMFVECCOVSSCVSSPPYCPQ-LDCGALHR 149
Db 154 CTR 156
Oy 150 HTR 152

RESULT 9
ID FASL_MOUSE STANDARD; PRT; 327 AA.
AC P25446;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148151.
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RT mouse Fas antigen.";
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE: 93189576.
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
RT transposable element in an intron of the Fas antigen gene of 1pr
RT mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [3]
RP VARIANT LPR.
RX MEDLINE: 92195401.
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis.";
RL Nature 356:314-317(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS

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CC LIVER, LUNG, HEART, AND ADULT OVARY.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC PRODUCTION.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M83649; AAA37593.1; -
CC EMBL: S56490; AAB25700.1; -
CC EMBL: S56485; AAB25700.1; JOINED.
CC EMBL: S56486; AAB25700.1; JOINED.
CC PIR: A46484; A46484.
CC HSP: P25445; IDPF.
CC MGD: MGI:95484; FAS.
CC PFAM: PF00020; TNFR_C6; 3.
CC PROSITE: PS00531; death; 1.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00050; TNFR_NGFR_2; 2.
CC PROSITE: PS50017; DEATH_DOMAIN; 1.
CC Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
CC Disease mutation.
CC KW SIGNAL 1 21
CC FT CHAIN 22 327 FASL RECEPTOR.
CC FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 170 186 POTENTIAL.
CC FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 43 162 3 X TNFR-CYS.
CC FT REPEAT 43 79 TNFR-CYS 1.
CC FT REPEAT 80 123 TNFR-CYS 2.
CC FT REPEAT 124 162 TNFR-CYS 3.
CC FT DOMAIN 222 306 DEATH DOMAIN.
CC FT CARBOHYD 43 43 POTENTIAL.
CC FT CARBOHYD 114 114 POTENTIAL.
CC FT VARIANT 246 246 I -> N (IN LPR).
CC SQ SEQUENCE 327 AA: 37418 MW: 68BFC5ACE356BEE CRC64;

Query Match 6.48; Score 204; DB 1; Length 327;
Best Local Similarity 27.9%; Pred. No. 4.35e-19;
Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;

DB 43 NCSEGLYGG-GPRCCQPCQPGKKKVEDCKKNNGGTPPCAPCTEGKEVMD-KNHVADKRCRC 100
- QY 34 DCAGDGHKKIGLFCRCPCGPHYLAKRCPGCGSTGLVCPQDT-FLAMENHNHSECARC 92
DB 101 TLDEEHGLEVETNCTLTONTCKCKRPDFCYDSPGCEHCYRCAS 144
- QY 93 QACDEQASQVALENCASVADTRCGCKPGMWVEQOVS-QCVSSSP 135

RESULT 10
ID FASA_HUMAN STANDARD; PRT; 335 AA.
AC P25445;
DT 01-MAY-1992 (rel. 22, Created)
DT 01-MAY-1992 (rel. 22, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95 ANTIGEN).
GN APT1 OR FAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91309137.

RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Saneshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis.";
RL Cell 66:233-243(1991).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE; 92268122.
RA Oelam A., Behnmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponsltingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/reverse growth factor
RT receptor superfamily. Sequence identity with the Fas antigen.";
RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RX STRUCTURE BY NMR OF 218-335.
RX MEDLINE; 97122332.
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL Nature 384:638-641(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NME-PROW; NOTE-CD guide CD95 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M67454; AAA63174.1; -
CC EMBL: X63717; CAA45250.1; -
CC PIR: A40036; A40036.
CC PIR: S24543; S24543.
CC PDB: 1DDF; 12-NOV-97.
CC MIM: 134637; -
CC PFAM: PF00020; TNFR_C6; 2.
CC PROSITE: PS00531; death; 1.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00050; TNFR_NGFR_2; 2.
CC PROSITE: PS50017; DEATH_DOMAIN; 1.
CC Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
CC 3D-structure.
CC KW SIGNAL 1 16
CC FT CHAIN 17 335 FASL RECEPTOR.
CC FT DOMAIN 17 173 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 174 190 POTENTIAL.
CC FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 47 166 3 X TNFR-CYS.
CC FT REPEAT 47 166 TNFR-CYS 1.
CC FT REPEAT 84 127 TNFR-CYS 2.
CC FT REPEAT 128 166 TNFR-CYS 3.
CC FT DOMAIN 230 314 DEATH DOMAIN.
CC FT CARBOHYD 118 118 POTENTIAL.
CC FT CARBOHYD 136 136 POTENTIAL.
CC SQ SEQUENCE 335 AA: 37732 MW: 0139942535111410 CRC64;

Query Match 5.9%; Score 190; DB 1; Length 335;

Best Local Similarity 34.1%; Pred. No. 2,226-16;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;
DB 56 GQFCCHKPCPGE-RKARDCTVNGDEPPCPCQEGKEYTD-KAHFSSKRCRRLCDEHGCL 113
QY 44 GLFCRCRCPAGHLYKAP-CTEPCGNSITLVCPODT-FLAMENHNHNSCARCOACDE-QAS 100
DB 114 EVEL-NCTRTONTKCRCKPNEFCNSTVCEHC 143
QY 101 QVALENCASAVADTRCGCKPWFVECOVS-QC 130
-RESULT 11
ID VRT.MYXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (Strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91335768.
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
necrosis factor receptor gene family that contributes to viral
virulence."
RT virulence."
RL virology 184:370-382(1991).
CC -I- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
REACH CELLULAR TARGET AND THEREBY DEAMENING THE POTENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC CC
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CC CC
DB EMBL; M95181; AAA46632.1; -
DB EMBL; A23729; CAA01688.1; -
DB PIR; A40566; GOVZML.
DR HSSP; P19438; TNFR.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT REPEAT 66 66 TNFR-CYS 4.
FT CARBOHYD 181 181 POTENTIAL.
FT CARBOHYD 205 205 POTENTIAL.
FT CARBOHYD 238 238 POTENTIAL.
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;
Query Match 5.7%; Score 182; DB 1; Length 326;
Best Local Similarity 30.9%; Pred. No. 7,376-15;
Matches 34; Conservative 23; Mismatches 45; Indels 8; Gaps 8;
DB 5 TLLIAYVACVGGGAPYAGDRKGRGNDYERKDL-CTCTCPGPGYSASRLCG-PGSPYVS 62
QY 14 ALLVLVIGARAGGTR-SP-RCDCAGDFHKKIGLFCRCRCPAGHLYKAPCTEPCGNSITL 71

DB 63 PCKNETFTA-STNHAPACVSCGRCTGHLSE-S-OSCDKTRDRCVDCSAG 109
QY 72 VCPDPTFLAMENHNHNSCARCOA-CDEQASQVALENCASVADTRCGCKRG 120
-RESULT 12
ID VC22.VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE; 93202281.
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
protective mechanisms."
RT FEMS Lett. 319:80-83(1993).
CC -I- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC CC
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or send an email to license@isb-sib.ch).
CC CC
DB EMBL; X69198; CAA49137.1; -
DB EMBL; X67117; CAA47540.1; -
DB PIR; D36858; D36858.
DR PIR; S35987; S35987.
DR PIR; S46888; S46888.
DR HSSP; P19438; TNFR.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Repeat.
FT DOMAIN 31 108 2 X TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D4SD40B5C6E780EF CRC64;
Query Match 5.6%; Score 179; DB 1; Length 349;
Best Local Similarity 27.1%; Pred. No. 2,706-14;
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7;
DB 15 IINGNDAPYIPPNCKKCDTER-KRHN-CLCSCEPGTYASLC-DSKNTQCTCGGSG 71
QY 18 VILGARAGGTRPRDCD-AGDFHKKIGLFCRCRCPAGHLYKAPCTEPCGNSITLVCPOD 76
DB 72 TETSRNNHL-PACLSGNGRGN-SNOVETRSCWTNTRICEGSPGY 115
QY 77 TFLAMENHNHNSCARCOA-CDEQASQVALENCASVADTRCGCKPWF 122
-RESULT 13
ID CD27.HUMAN STANDARD; PRT; 260 AA.
AC P26842;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD27 RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14).
GN TNFRSF7 OR CD27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MONOCYTES:
RX MEDLINE: 92013149.
RA Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
RT "The T cell activation antigen CD27 is a member of the nerve growth
RT factor/tumor necrosis factor receptor gene family.";
RL J. Immunol. 147:3165-3169(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93094588.
RA Loenen W.A., Gravelstein L.A., Beumer S., Melief C.J., Hagemeijer A.,
RA Borst J.;
RT "Genomic organization and chromosomal localization of the human CD27
RT gene.";
RL J. Immunol. 149:3937-3943(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
CC -1- A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.
CC -1- PTM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD27 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63928; AAA58411.1; -.
DR PIR: A46454; A46454.
DR PIR: A46517; A46517.
DR HSSP: P19438; INCF.
DR MIM: 166711; -.
DR PIR: P00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 260 CD27L RECEPTOR.
FT DOMAIN 21 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 212 POTENTIAL.
FT DOMAIN 213 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 141 3 X TNFR-CYS.
FT REPEAT 26 63 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 POTENTIAL.
FT MOD_RES 219 219 PHOSPHORYLATION (POTENTIAL).
FT CONFLICT 59 59 A -> T (IN REF. 2).
SO SEQUENCE 260 AA; 29156 MW; 43C38B92FA90DME2 CRC64;

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Query Match 5.48; Score 174; DB 1; Length 260;
Best Local Similarity 25.48; Pred. No. 2,32e-13;
Matches 31; Conservative 34; Mismatches 48; Indels 9; Gaps 7;

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RESULT 14
ID ID TNFR2_HUMAN STANDARD: PRT; 461 AA.
AC P20333.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 2) (TNFR2) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90260639.
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91045991.
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96299745.
RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepassier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE: 90349572.
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE: 90110215.
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE: 91036048.
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE: 93016040.
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.

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RX MEDLINE: 99221490.
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
 APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACOLOGICAL: AVAILABLE UNDER THE NAME EMBREL (IMMUNEX AND
 MYERH-AERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 ARTHRITIS (RA). EMBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
 CC -1- DATABASE: NAME-Embrel; NOTE-clinical information on Embrel;
 WWW="http://www.embrelinfo.com/".
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 CC -----
 DR EMBL: M33315; AAA59929.1; -;
 DR EMBL: M35857; AAA63262.1; -;
 DR EMBL: U52165; AAC50622.1; -;
 DR EMBL: U52156; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA36755.1; -;
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -;
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KM Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 258 287 POTENTIAL.
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 201 4 X TNFR-CYS.
 FT REPEAT 39 76 TNFR-CYS 1.
 FT REPEAT 77 118 TNFR-CYS 2.
 FT REPEAT 119 162 TNFR-CYS 3.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT REPEAT 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 73 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.

FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 POTENTIAL.
 FT CARBOHYD 193 193 POTENTIAL.
 FT CONFLICT 141 141 R -> P (IN REF. 4).
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
 FT CONFLICT 363 363 A -> T (IN REF. 4).
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;
 Query Match 5.3%; Score 168; DB 1; Length 461;
 Best Local Similarity 27.6%; Pred. No. 2,97e-12;
 Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;
 Db 44 EYDPTAACCSCSKSPGHAKVCTKT-SDTVCSCEDESTYQLM-NW-VPECLSCGSRG 100
 Qy 38 DEHKHIGLFCGCGPAGHYLKPCTEPCGNSYCLVPODTFLA-WENHNHNSCARCOA-C 95
 Db 101 S-SQVETQACTRQNRNCTCRPMY 125
 Qy 96 DEQASVALENCASAVADTRCGCKPGWF 122
 RESULT 15
 ID OX40_RAT STANDARD; PRT; 271 AA.
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
 GN TXGPIL OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-T-CELL.
 RX Medline: 90214614.
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
 lymphocytes -- a molecule related to nerve growth factor receptor.";
 RL EMBO J. 9:1063-1068(1990).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
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 CC -----
 DR EMBL: X17037; CAA34897.1; -;
 DR PIR: S08036; S08036.
 DR PIR: S12783; S12783.
 DR HSP: P25942; ICDF.
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 KM Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 271 OX40L RECEPTOR.
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 235 POTENTIAL.
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 164 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 102 TNFR-CYS 2.
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 124 164 TNFR-CYS 4.
 FT CARBOHYD 143 143 POTENTIAL.

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Mparch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 25 22:24:16 2000; Maspar time 23.31 seconds
 Tabular output not generated. 843.833 Million cell updates/sec

Title: >US-09-314-889-4
 Description: (1-417) from US09314889.pep
 Perfect Score: 3198
 Sequence: 1 MEQRRCGAAYAAALLLVLL.....ERMGIDGCVEDLRSLQKCP 417

Scoring table:
 PAM 150
 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r64
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 47.731; Variance 92.974; scale 0.513

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description	Pred. No.
1	407	12.7	455	1 G0HUT1	tumor necrosis factor
2	399	12.5	454	1 G0MST1	tumor necrosis factor
3	398	12.4	461	2 JC4302	tumor necrosis factor
4	385	12.0	454	2 157826	tumor necrosis factor
5	383	12.0	461	1 G0RT1	tumor necrosis factor
6	211	6.6	324	2 JC2395	Fas antigen precursor
7	204	6.4	327	2 A46484	apoptosis-mediating m
8	190	5.9	314	2 137383	FAS soluble protein
9	190	5.9	335	2 A40036	apoptosis-mediating s
10	182	5.7	326	1 G0V2ML	T2 protein - myxoma v
11	179	5.6	349	2 D36858	gene G4R protein - va
12	174	5.4	260	1 A46517	CD27 antigen precursor
13	168	5.3	461	1 A35356	tumor necrosis factor
14	165	5.2	271	1 A32783	OX40 antigen precursor
15	164	5.1	325	2 B43692	T2 protein - rabbit f
16	160	5.0	272	2 148700	gene OX40 protein - m
17	159	5.0	277	2 A60771	B-cell activation pro
18	160	5.0	435	2 154182	tumor necrosis factor
19	161	5.0	474	2 B38634	tumor necrosis factor
20	157	4.9	250	1 A49053	CD27 antigen precursor
21	157	4.9	250	1 A48854	gene murine tumor ne
22	153	4.8	656	2 149299	receptor interacting
23	146	4.6	416	1 JN0006	nerve growth factor r

24	139	4.3	427	1 G0HUN	nerve growth factor r
25	134	4.2	372	2 I38992	receptor interacting
26	134	4.2	671	2 T09479	serine/threonine prot
27	131	4.1	425	1 A26431	nerve growth factor r
28	125	3.9	132	2 S57566	Fas/Apo-1/CD95 protei
29	125	3.9	149	2 S58662	Fas-Delta-(4,7) prote
30	124	3.9	1808	2 T15099	hypothetical protein
31	124	3.9	3635	2 T10053	laminin alpha-5 chain
32	121	3.8	1574	2 T13954	MEGF6 protein - rat
33	117	3.7	407	2 C70816	hypothetical protein
34	114	3.6	277	2 I37552	OX40 homolog - human
35	116	3.6	799	2 A38308	integrin beta-5 chain
36	114	3.6	1247	1 MMHUND	nidogen precursor - h
37	111	3.5	656	2 JC2005	integrin beta-5 chain
38	111	3.5	1607	1 MMMSB2	laminin gamma-1 chain
39	112	3.5	1609	1 MMHUB2	laminin gamma-1 chain
40	108	3.4	103	2 A42523	A53R protein - vaccin
41	110	3.4	289	2 A46515	B cell-associated sur
42	110	3.4	305	2 A46476	CD40 - mouse
43	109	3.4	571	2 C75165	glutanyl-tRNA synthet
44	109	3.4	1790	1 MMFPB1	laminin beta-1 chain
45	109	3.4	3707	2 S18252	heparan sulfate prote

ALIGNMENTS

RESULT	1	ALIGNMENTS
ENTRY	G0HUT1	#type complete
TITLE	tumor necrosis factor receptor 1 precursor - human	
ALTERNATE_NAMES	P55 tumor necrosis factor receptor; TNF receptor	
CONTAINS	tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor)	
ORGANISM	#formal_name Homo sapiens #common_name man	
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999	
ACCESSIONS	A38208; A34899; A34900; A36555; A38281; S12057; J07058; A60231; A38258; A60594; A35010; JC2404	
REFERENCE	A38208	
#authors	Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.	
#journal	Genomics (1992) 13:219-224	
#title	Structure of the human TNF receptor 1 (p50) gene (TNRF1) and localization to chromosome 12p13.	
#cross-references	MUID:92250049	
#accession	A38208	
#molecule_type	DNA	
#residues	1-455 #label FUC	
#cross-references	GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g339750	
REFERENCE	A34899	
#authors	Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.	
#journal	Cell (1990) 61:351-359	
#title	Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.	
#cross-references	MUID:90235284	
#accession	A34899	
#molecule_type	mRNA	
#residues	1-455 #label LOE	
#cross-references	GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754	
#experimental_source	part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing	
#note		
REFERENCE	A34900	
#authors	Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.	
#journal	Cell (1990) 61:361-370	
#title	Molecular cloning and expression of a receptor for human tumor necrosis factor.	
#cross-references	MUID:90235285	
#accession	A34900	
#molecule_type	mRNA	

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##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:9339744; PIDN:AA03210.1; PID:9339745
REFERENCE
#authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
#journal Pflanzmaler, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
#title DNA Cell Biol. (1990) 9:705-715
#cross-references MUID:91090841
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:9339755; PIDN:AAA6754.1; PID:9339756
#accession C36555
##molecule_type protein
##residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
#note 107-128;162-167,'X',169-201 ##label H12
the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor
REFERENCE
#authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
#cross-references GB:M37764
#note the authors translated the codon TGG for residue 371 as
Thr, AAG for residue 372 as Leu, and GAC for residue
427 as Asn
REFERENCE
#authors Nophr, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
#journal R.; Aderka, D.; Holtmann, H.; Wallach, D.
#title EMBO J. (1990) 9:3269-3278
Solid forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:91006021
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NOP
#cross-references EMBL:X55313; NID:937223; PIDN:CAA39021.1; PID:937224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing
REFERENCE
#authors JT0758
#journal Kemper, O.; Wallach, D.
#title Gene (1993) 134:209-216
Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#cross-references MUID:94085779
#accession JT0758
##molecule_type DNA
##residues 1-13 ##label KEM
REFERENCE
#authors A60231
#journal Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
#title J.M. Immunol. (1990) 20:1167-1174
Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
#residues 41-43,'X',45-53,'X',55-57 ##label SEC
REFERENCE
A38258

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```

#authors Gatana, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III,
#journal J.A.; Jeffers, E.W.B.; Lantz, R.; Tomich, J.; Yamamoto,
#title R.S.; Granger, G.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
Purification and characterization of an inhibitor (soluble
tumor necrosis factor receptor) for tumor necrosis factor
and lymphotoxin obtained from the serum ultrafiltrates of
human cancer patients.
#cross-references MUID:91062364
#accession A38258
##molecule_type protein
##residues 41-60 ##label GAT
#cross-references MUID:91062364
#experimental_source cancer patient serum
REFERENCE
#authors A60594
#journal Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
#title Grubb, A.; Adolf, G.
Eur. J. Haematol. (1989) 42:270-275
Isolation and characterization of a tumor necrosis factor
binding protein from urine.
#cross-references MUID:89171156
#accession A60594
##molecule_type protein
##residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
#cross-references MUID:90110215
#accession A35010
##molecule_type protein
##residues 41-45 ##label ENG
#cross-references MUID:90110215
#experimental_source normal urine
REFERENCE
#authors JC2404
#journal Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#title Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#cross-references MUID:95128033
#accession JC2404
##molecule_type protein
#residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
#label KAJ
#experimental_source urine
COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).
GENETICS
#gene GDB:TNFR1
#cross-references GDB:125913; OMIM:191190
#map_position 12p13.2-12p13.2
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-21
22-455
#domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 1 #status
predicted #label MAT\
#domain extracellular #status predicted #label EXN\
#product TNF binding protein 1 (tumor necrosis factor
alpha inhibitor) #status experimental #label TBP1\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label MEM\
#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY
#length 455 #molecular-weight 50494 #checksum 153

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				Gaps 32
Db	27	VIGLVPHLGRERKDSVPGGKGIHPONNSICCKKCKGTLYLNDKPGPGDTCRECES	86	
OY	19	LLGARAGGGRSR - CDCA - GDF - HKKIGLFCRCGCGAGHTLAKPTCEPGNSICLYCPQ	75	
Db	87	GSFTASENHLR - HCLSCSKCKEMGOYEISSCTVDRDTCGCRKQYRHYW - SENLFOC -	143	
OY	76	DFPLAMENHNHNSCARQACDPOASGYALBNCSAVATPTCGCKRGWVECGVSQCVSSP	135	
Db	144	FNCSLCLN - CTIV - --- - LSCQEKONTYC - TCHAGFEI - RENECVSCSNCKSLCTKICLCP	197	
OY	136	FCYCPCLDGCALHRRHRLIC - SRRDDDCGCLCPDFYEHGGCVCSPTSTIG - SCPERC - A	192	
Db	198	QIENVKGTEDSGTYLLP - LVIFEGCLCLLFLGLMYRQRMKSKITSLYCGKSTPEKE	256	
OY	193	AVCGHQM - W - VOVLLAGLV - - PL - LLCATLT - YTYR - HCWPHK - - PLVTADEA - GME	242	
Db	257	GELEGTTRPLADNPSPSPGCTPTLGFSPVPSSTPTSSSTYVPGDCPNFAARREYAP	316	
OY	243	A - LTPPAPHTLSPDLS - AHTL - LAPDSSSEKICITGLVGN - WTPGVPEHGCALCPQYT -	297	
Db	317	PYGAPPIATALASDPPIPPLOKMEBSAKRPOSJTDPPATLYAAVENPPLMKFEVR	376	
OY	298	- W - SMDPLSRALGPAAP - LSP - ESPASSPAMLOPGFO - LYDVMDAVPARMKFEVR	352	
Db	377	RGLSHEIDRLRLONGRCLEAOYSMLATWRRTPREATLELGLVLRMDLGGLED	436	
OY	353	TIGLRAREIEAVEVEIGR - FRDOOYEMLRKWRQOP - - AGLCAVYALBERMGIDGVED	408	
Db	437	IEPAL 441		
OY	409	LRSRL 413		
RESULT 2				
ENTRY	GOMST1	#type complete		
TITLE	tumor necrosis factor receptor 1 precursor	- mouse		
ALTERNATE_NAMES	tumor necrosis factor receptor, 55k			
ORGANISM	#formal_name Mus musculus	#common_name house mouse		
DATE	30-Jun-1992	#sequence_revision 30-Jun-1992	#text_change 22-Jun-1999	
ACCESSIONS	A38634	B40254	S16677	S19021
REFERENCE	A38634			
#authors	Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.			
#journal	Proc. Natl. Acad. Sci. U.S.A.	(1991) 88:2830-2834		
#title	Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.			
#cross-references	MUID:91187885			
#accession	A38634			
#molecule_type	mRNA			
#residues	1-454	#label LEW		
#cross-references	GB:M60468	NID:g199825	PIDN:AAA39751.1	PID:g199826
REFERENCE	A40254			
#authors	Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.T.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.			
#journal	Mol. Cell. Biol.	(1991) 11:3020-3026		
#title	Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.			
#cross-references	MUID:91246168			
#accession	B40254			
#molecule_type	mRNA			
#residues	1-454	#label GO2		
#cross-references	GB:M60468	NID:g199825	PIDN:AAA39751.1	PID:g199826
REFERENCE	S16677			
#authors	Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.			
#journal	Eur. J. Immunol.	(1991) 21:1649-1656		
#title	Cloning, expression and cross-linking analysis of the murine			

Accession	Protein Name	Species	Length	Score	DB	Length	Score	DB
#cross-references MUID:91285014	p53 tumor necrosis factor receptor.	Human	302	12.5%	Score 399;	DB 1;	Length 454;	
#accession S16677		Human	302	Best Local Similarity	28.7%;	Pred. No. 2,92e-53;		
#molecule_type mRNA				Matches 119;	Conservative 79;	Mismatches 182;	Indels 34;	Gaps 28;
#residues 1-454	#label BAR							
#cross-references EMBL:559238;	NID:953578;	PIDN:CAA41922.1;	PID:953579					
REFERENCE S19021								
#authors Rothe, J.G.;	Brockhaus, M.;	Gentz, R.;	Lesslauer, W.					
#journal Immunogenetics (1991) 34:338-340								
#title Molecular cloning and expression of the mouse Tnf receptor type b.								
#cross-references MUID:92039815								
#accession S19021								
#molecule_type mRNA								
#residues 1-454	#label ROT							
#cross-references EMBL:557796;	NID:954848;	PIDN:CAA40936.1;	PID:954849					
REFERENCE S15532								
#authors Bebo, B.F.								
#journal Nucleic acid research (1994) 22:450-451								
#title Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.								
#cross-references MUID:94245292								
#accession S15532								
#status translated from GB/EMBL/DBJ								
#molecule_type mRNA								
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#cross-references GB:I26349;	NID:9430732;	PIDN:AAA59361.1;	PID:94307333					
COMMENT TNF-alpha (cachectin) and TNF-beta (lymphotoxin).								
CLASSIFICATION	#superfamily tumor necrosis factor receptor type 1;	NGF receptor repeat homology						
KEYWORDS	duplication; glycoprotein; receptor; transmembrane protein							
FEATURE								
1-29	#domain signal sequence	#status predicted	#label SIG\					
30-454	#product tumor necrosis factor receptor type 1	#status predicted	#label MAT\					
30-212	#domain extracellular	#status predicted	#label EXT\					
44-82	#domain NGF receptor repeat homology	#label NG1\						
84-136	#domain NGF receptor repeat homology	#label NG2\						
127-167	#domain NGF receptor repeat homology	#label NG3\						
168-204	#domain NGF receptor repeat homology	#label NG4\						
213-235	#domain transmembrane	#status predicted	#label MEM\					
236-454	#domain intracellular	#status predicted	#label INT\					
54,151,202	#binding-site carboxylate (Asn) (covalent) #status predicted							
SUMMARY	#length 454	#molecular-weight 50129	#checksum 4839					
Query Match	12.5%;	Score 399;	DB 1;	Length 454;				
Best Local Similarity	28.7%;	Pred. No. 2,92e-53;						
Matches 119;	Conservative 79;	Mismatches 182;	Indels 34;	Gaps 28;				
Db	40	RDSICP-OGKVVHKKNNISICTKHKNTYLVSDPSRGRTVCRECKGFTASQWYLR	97					
29	RSPRDCDAGDE-HKKIGLFCRCGRPAHNYLKAPDTECGSTLVCPCQDFLAMEHHNS	87						
98	QCLSKTCRKMSQVEISPCQADKDYCGCKENOFYRLSETHFQCVCSPCFNGTPTP	157						
88	ECARQADDBASQVALENCASAVADTKCGCKPGRFVRC--QVS-QCYSSSP-FYQCPCLD	143						
158	CKETQ-NTVCNCHAGFLRESEVPC--SHCKNEBCMKLCPLPLANTVTPNODSGTAVL	214						
144	CGALHRTLRILC-SR---RDTDCGTCPLRGFEHDDGVS-CPTSLTSC--PERCAAVCG	196						
215	LPVILGLCLLSTFLFSLMKRYRMKRPVYSSICRPPV-VKEBKAGK-PLTPASPAF	272						
197	WRQMWQV-LLAGLVPL-LTGLT-LTYTYR-CWNHKPLVADAEKGMPPATPH	252						
273	SPSGFNFTLCFSPGSSPVSSP-ISPFGSPSMHFMPPVSEVPTQCADLLESIC	331						
253	SPDS-ATTL-LAPDSSSEKICTYQVLGNSMTPEYPTQALCPQV-TNSMDLPSRAIG	309						
332	SVPAFTSVQKWEASHPDRPDNADLALIVAVDGVPPARKKEMRMGSLSEHIERLEMG	391						

QY 310 PAAAPTLPSPSPAGS-PAMMLQPG-POLYDVMDAVPARMKFEVETLGLREAEIEAVEVE 367

Db 392 NGRCLEAOXSMLAMRRRRPRRHEDTLEVGLVSKMLACLENIILAL-RNP 444

QY 368 IGR-FRDOQYEMLRKRWROOP--AG-LGAVYAALERMGIDGVEDLRSRLQGRP 417

RESULT 3

ENTRY JC4302 #type complete

TITLE tumor necrosis factor receptor p55 precursor - pig

ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig

DATE 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999

ACCESSIONS JC4302; PC4093

REFERENCE JC4302

#authors Suter, B.; Pauli, U.

#journal Gene (1995) 163:263-266

#title Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

#cross-references MUID:96011645

#accession JC4302

#molecule_type mRNA

#residues 1-461 ##label SUR

#cross-references GB:U1994; NID:9141752; PIDN:AC48499.1; PID:g1141753

#accession PC4093

#molecule_type protein

#residues 1-7 ##label SU2

#experimental_source kidney cell line 15

GENETICS

#gene tnfr

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor

FEATURE

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44-194

44-82

84-126

211-231

361-447

54,145,151

SUMMARY #length 461 #molecular_weight 50696 #checksum 8079

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Best Local Similarity 32.3%; Pred. No. 4,61e-53;

Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

Db 33 HPRGRKRESICPGQKYSHPNRSICCTCKHKGYTLHANDCLAGIDTCRECDNFTFAS 92

QY 25 QGGTRSPR-CDCA-GDF-HKRTGLFCRCGCPAGHLYLAKPCTEPCGNSCLVCPDPTFLAM 81

Db 93 ENHT-TGCLSCSKRSEKSOYEISPCVTDRDVTGCGCRKN--QYR-KY-NSETLF-Q-C 143

QY 82 ENHNNSCARQACDEQASQVALENCSAVADTRCGCKPGMYECCOVSOCVSSPFYCQPC 141

Db 144 LNC-SLCPNGTVQPLCEKODTICN-CHSGFLRDKECVSCVNCNADCKNLCPATSETR 201

QY 142 LDGCLALRH-T-RLLC-SRDPDGTCLPGFYEHGDCGVSCPTSLTSGCPRECAVCMGR 198

Db 202 NDPODTGTVLLPLVIFGLCLAFPLVGLACRIOR-WKPKLYSITIGSKSPYKGEPEP 260

QY 199 QMEF---VOYILA-----GLVVPPLILGATLYTYRHCWPHK--PLY---TA-DEAGMEA 243

Db 261 LATAPSGPITTFSPISPTTFSPVPSPISSPTFTCDMSNITVTSPPKRIAPP 320

QY 244 L-TTP---PALTHSPUDS-AHTL-LAPDSSSKICTVOLVGNSTWTP---GIPETDEALCP 294

Db 321 QGAGPILMPAPSTVPPLPRKMGSAHSAPQALDADPATLYAVDGPPTRMKEF 380

QY 225 QYTWMDQLP-SRALGPAAAPTL--SPSPAGSPAMMLQPGPQ-LYDVMDAVPARMKKEF 350

Db 381 VRRLLSEHIEIRLELQNGRCLEAOXSMLAEWRRTSREKTELELIGSLADMDLGL 440

QY 351 VRTGLREAEIEAVEVEIGR-FRDOQYEMLRKRWROO--OP-AGLAVYAALERMGIDGCV 406

Db 441 EDIEEAL-RGP 450

QY 407 EDLRSRLQGRP 417

RESULT 4

ENTRY 157826 #type complete

TITLE tumor necrosis factor receptor - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

ACCESSIONS 157826

REFERENCE 157826

#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

#journal Mol. Immunol. (1993) 30:165-176

#title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

#cross-references MUID:93156721

#accession 157826

#status preliminary; translated from GB/EMBL/DBDJ

#molecule_type DNA

#residues 1-454 ##label RES

#cross-references GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102

GENETICS

#gene TNFR-2

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

KEYWORDS cytokine receptor

FEATURE

44-82

SUMMARY #length 454 #molecular_weight 50030 #checksum 4267

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Best Local Similarity 28.5%; Pred. No. 1,68e-50;

Matches 118; Conservative 79; Mismatches 183; Indels 34; Gaps 28;

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QY 29 RSPRCDACGDF-HKRTGLFCRCGCPAGHLYLAKPCTEPCGNSCLVCPDPTFLAMENHNS 87

Db 98 QCLSGCTCKREMSQYEISPCQADKDTVCGCKENQFORLYSETHFQVDCSPGFNGTVTP 157

QY 88 ECARQACDEQASQVALENCSAVADTRCGCKPGMYECC--QYS-QCVSSP-FYCQPCID 143

Db 158 CKETO-NIVCNCHAGFLESECVPC--SHCKNNECMKLCPLRPPLANTNPQDSTAVL 214

QY 144 CGALRHNRRLC-SR---RDTCGTCILPGFYEHGDCVCS-CPTSLTSGSC--PERCAAYCG 196

Db 215 LPLVILIGLCLSFIFISIMCYPRMRREYVSTIGCDPRP-VKEEKAG-PLTPAPSPAF 272

QY 197 WRQMFVVOY-LIAGLVVPL-LGATL-TYTYRH-CWRHRLVTADAGMALPRPATYH 252

Db 273 SPTSGFNPLPGFSPGFSSPVASTP-ISPFGPSNMHFMPPVSEVVPYTGADPLYLESLC 331

QY 253 SPLDS-AHTL-LAPDSSSKICTVOLVGNSTWTPGYETDEALCPQV-TSMWQLPBRAG 309

Db 332 SVAPLTVQKWDASHPQRPDADALIAIVVDGVPAPAKEMRPMGLSEHIEIRLEAQ 391

QY 310 PAAAPTLPSPSPAGS-PAMMLQPG-POLYDVMDAVPARMKFEVETLGLREAEIEAVEVE 367

Db 392 NGRCLEAOXSMLAMRRRRPRRHEDTLEVGLVSKMLACLENIILAL-RNP 444

QY 368 IGR-FRDOQYEMLRKRWROOP--AG-LGAVYAALERMGIDGVEDLRSRLQGRP 417

```

RESULT      5
ENTRY       5
TITLE       GQRTT1      #type complete
CONTAINS    tumor necrosis factor receptor 1 precursor - rat
ORGANISM    #formal_name Rattus norvegicus #common_name Norway rat
DATE        30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
ACCESSIONS  B36555
REFERENCE    A36555
#authors     Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
#journal     Pflümaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
#title       DNA Cell Biol. (1990) 9:705-715
#cross-references GB:M63122; NID:g207361; PIDN:AAA4256.1; PID:g207362
#accession   B36555
#molecule_type mRNA
#residues    1-461 ##label HIM
#cross-references GB:M63122; NID:g207361; PIDN:AAA4256.1; PID:g207362
COMMENT      This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
KEYWORDS       receptor repeat homology
FEATURE        duplication; glycoprotein; receptor; transmembrane protein
1-29
30-461
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30-201      #product tumor necrosis factor receptor type 1 #status
              predicted #label MAT\
              #domain extracellular #status predicted #label EXT\
              #product tumor necrosis factor binding protein #status
              predicted #label TBP\
44-82      #domain NGF receptor repeat homology #label NG1\
84-126      #domain NGF receptor repeat homology #label NG2\
127-167      #domain NGF receptor repeat homology #label NG3\
168-204      #domain NGF receptor repeat homology #label NG4\
212-224      #domain transmembrane #status predicted #label MEM\
235-461      #domain intracellular #status predicted #label INT\
54,151,201   #binding_site carboxydrate (Asn) (covalent) #status
              predicted
SUMMARY       #length 461 #molecular-weight 50969 #checksum 1617

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Best Local Similarity 29.8%: Pred. No. 4,15e-50;
Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;

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      27 GTRSPKCD-CA-GDF-HKKTGLFCCKRCRPAHLYLKAPCTEPCGSLTCLVCPDFFLWEN 83
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      95 H-VROGLSCKTCKREKMEVOEISPCAKDMDTVCGCKKNQFORYLETHFQCVDSPCENGT 153
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      84 HHNSRCARCOAQEOQASQVALENCASAVADRCKGCKPGWFECC--QVS-QCVSSSP-FYCO 139
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      154 VTIPECK-KONTVCNCHAGFLLSGNECTPCSHCKKNOECKLCLPRVANTNPQDSTAV 212
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      213 LRLVFLGLCLFLFCISILCLRYQWRRPRVYIICRDSAPVEVEBEGLVTKPLTPASTI 272
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      196 GWRQRMWVOV-LIAGLVPLL--LGATLYTYRH-CWPHKPLVTADAGM--EALTPPPA 249
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      273 PAFSPNGENPTLGFSTTPRFSHPVSTPISPVGFSPNMHNPVRYEVPTQ-G-A-DP 329
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      250 THLSPLDS-AHTL-LAP-PDSSEKICTYOL-V-GNS-WTPGVPENQALCPQVTSWMDQ 302
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      330 LLYGSLNPVPIPAFVKWEDYVAAQORLDTADPAMLYAVVGVPPTRKMEKRLGLSE 389
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      303 LPSRALGPAAAPT-LSP-ESPAGSPAMMLQPG-PO-LYDVMADVAPARRMKEFEVTLGLRE 358
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT      6
ENTRY       JC2395
TITLE       Fas antigen precursor - rat
ORGANISM    #formal_name Rattus norvegicus #common_name Norway rat
DATE        20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
ACCESSIONS  JC2395; PC2246
REFERENCE    JC2395
#authors     Kimura, K.; Wakatsuki, T.; Yamamoto, M.
#journal     Biochem. Biophys. Res. Commun. (1994) 198:666-674
#title       A variant mRNA species encoding a truncated form of Fas
              antigen in the rat liver.
#cross-references MUID:94128114
#accession   JC2395
#molecule_type mRNA
#residues    1-324 ##label KIM
#cross-references DBJ:D26112; NID:g468486; PID:d1005650; PID:g468487
#experimental_source thymus
#accession   PC2246
#molecule_type mRNA
#residues    1-62, 'RFR' ##label KIZ
#cross-references DBJ:D26113; NID:g468488; PID:d1005651; PID:g468489
#experimental_source liver
GENETICS     #introns 62/1
CLASSIFICATION #superfamily NGF receptor repeat homology
KEYWORDS       transmembrane protein
FEATURE        1-21
22-324      #domain signal sequence #status predicted #label SIG\
44-79      #product Fas antigen #status predicted #label MAT\
81-124      #domain NGF receptor repeat homology #label NG4\
171-188      #domain transmembrane #status predicted #label TMM
SUMMARY       #length 324 #molecular-weight 36835 #checksum 7305

Query Match      6.1%: Score 211; DB 2; Length 324;
Best Local Similarity 30.1%: Pred. No. 8,54e-18;
Matches 37; Conservative 26; Mismatches 47; Indels 13; Gaps 12;

Db      43 NCSEGLIY-VSPFCQPCQGEERKVKD-CTTSGAPTCPTCEBEYTDK-KHYSKCR 99
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      34 DCADDFHKKIGLFCRCRCPAG-HYLKAPCTEPCGNSITCLVCPQ-DTFLAWENHHNSCAR 91
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      100 CAFEDEGHLEVE-TNCRTRQNTCRCKENFY--CNAISLC-DHC-YHCTSGCLE-DLEP 153
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      92 CQACDE-QASQVVALENCASAVADRCKGCKPGWFEVCOVSSSPFYCPC-LDCGALHR 149
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      154 CTR 156
      1 1
      150 HTR 152

RESULT      7
ENTRY       A46484
TITLE       apoptosis-mediating membrane-associated polypeptide Fas -
              mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS  A46484; A47254
REFERENCE    A46484
#authors     Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;
              Copeland, N.G.; Jenkins, N.A.; Nagata, S.
#journal     J. Immunol. (1992) 148:1274-1279
#title       The cDNA structure, expression, and chromosomal assignment of
              the mouse Fas antigen.
#cross-references MUID:92148151
#accession   A46484

```

```

##status      preliminary
##molecule_type mRNA
##residues    1-327 ##label WAT
##cross-references GB:M35645; NID:9193225; PTD:9193226
##experimental_source BMS3 macrophage cell line
##note        sequence extracted from NCBI backbone (NCBIN:81544,
               NCBIR:81545)

REFERENCE
#authors      A47254
#journal      Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
#title        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
               Aberrant transcription caused by the insertion of an early
               transposable element in an intron of the Fas antigen gene
               of lpr mice
#cross-references M01D:93189576
#accession    A47254

##status      preliminary
##molecule_type nucleic acid
##residues    1-96 ##label ADA
##cross-references GB:S56490; NID:9298505; PTD:9298506
##experimental_source MRL lpr/lpr
##note        sequence extracted from NCBI backbone (NCBIN:126850
               NCBIN:126853, NCBIR:126864)

CLASSIFICATION
#superfamily NGF receptor repeat homology
#transmembrane protein

FEATURE
44-79         #domain NGF receptor repeat homology #label NGF\
81-124        #domain NGF receptor repeat homology #label NG4

SUMMARY
#length 327  #molecular_weight 37417  #checksum 8479

```

Query Match	6.48;	Score 204;	DB 2;	Length 327;
Best Local Similarity	27.9%;	Pred. No. 1.42e-16;		
Matches	29;	Conservative	52;	Indels 4; Gaps 4,

[illegible]

```

RESULT      8
ENTRY
TITLE       I37383      #type complete
            FAS soluble protein - human
            #formal_name Homo sapiens #common_name man
            02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
            02-Jul-1996
DATE

```

ACCESSIONS 137383
 REFERENCE 137383
 #authors Cascino, I.; Finucci, G.; Papoff, G.; Ruberti, G.
 #journal J. Immunol. (1995) 154:2706-2713
 #title Three functional soluble forms of the human
 apoptosis-inducing Fas molecule are produced by alternative
 splicing.

```

#status      preliminary: translated from GB/EMBL/DB/
#molecule_type  rRNA
#residues      1-314  ##label  RRS
#cross-references  EMBL:z47853; NID:g728578; PTD:g695539
#length        314  #molecular_weight 35386  #checksums
SUMMARY

```

Query Match	5.9%;	Score 190;	DB 2;	Length 314;
Best Local Similarity	34.1%;	Pred. No. 3.60e-14;		
Matches	31;	Conservative	18;	Mismatches 35;
			Indels	7;
			Gaps	7;

Db 56 GQFCHKPCPEE-RKARDCTVNGDEPDYCPQEGKEAYTD-KAHSSCKRRRLCDEGHG 113
|||::|||::|||::|||::|||::
QY 44 GLPCCRGCPCAGHYLKAP-CTEPGCGNSTCLVCPQDT-FLAMENHHNSECARQACDE-QAS 100

```
Db      114 EVEI-NCTRQTCKRCRKPNEFCNSTVCEHC 143
      :| : || : :| : ||| | : | :|
```

QY 101 QVALENCASAVADTRCGCKPGWFEQVS-QC 130

RESULT	ENTRY	9
	A40036	#type complete
		apoptosis-mediating surface antigen Fas precursor - human
		surface antigen Apo-1
		#formal_name Homo sapiens #common_name man
		17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
		10-Sep-1997

#authors
 ACCESSIONS
 A40036; S24543; A38142
 REFERENCE
 A40036
 Titb N : Yonehara, S.; Tshji, A.; Yonehara, M.; Mizushima

#journal S. I. : Samehshina, M. : Hase, A. : Seto, Y. : Nagata, S.
#title Cell (1991) 66:233-243
The polypeptide encoded by the cDNA for human cell surface
antigen Fas can mediate apoptosis.
#cross-references M01D:91309137

```
##status      preliminary
##molecule_type  mRNA
##residues      1-335  ##label  ITO
##crotoss-references  GB:M6745;  NID:q182409;  PID:q182410
REFERENCE      S24543
```

```
#submission submitted to the EMBL Data Library, February 1992
#accession S24543
#status preliminary
```

```

#residues      1-335  #label KRA
#cross-references EMBL:X63717; NID:g28741; PID:g38742
REFERENCE
A38142
Cohen A. , Robertson T. , Eddy W. , Davlita

```

#Journal #Title	#Author
100368103	Verma, A.; Behrmann, J.; Fink, A.; Karsan, A.; Klagsbrun, M.; Rapp, U.H.; Schaeuble, C.; Weber, W.; Reichs, S.; Dhein, J.; Trauth, K.A.; Ponsling, H.; Gramlich, P.H. J. Biol. Chem. (1993) 267:10709-10715
100368104	Purification and molecular cloning of the Apo-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen

```
##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-134,'Q',136-335 ##label OE8
##experimental_source SKM6.4 cells
##note
##note sequence extracted from NCBI backbone (NCBIRef:103810)
##note In NCBI backbone the source is designated as mouse
```

```
#gene      GDB:APR1
#cross-references GDB:132671; OMIM:134637
#map_position 10q24.1-10q24.1
CLASSIFICATION #superfamily NGF receptor repeat homology
KEYWORDS      apoptosis; surface antigen; transmembrane protein
FEATURE
```

85-128	#domain	NGF receptor repeat	homology	#label	NG4\	
174-190	#domain	transmembrane	#status	predicted	#label	TMM
SUMMARY	#length	335	#molecular-weight	37732	#checksum	4899

Query Match	5.9%;	Score 190;	DB 2;	Length 335;
Best Local Similarity	34.1%;	Pred. No. 3.60e-14;		
Matches	31;	Conservative	18;	Mismatches 35;
			Indels	7;
			Gaps	7;

Db 56 GQFCHKPCPGE-RKARDCTVNGDEPDVCPCQEKEYTD-KAHSSKCRRCRLCDEGHGL 113
| | : | : | | : | : | : | : | : | : | :
QY 44 GLFCGCGCPAGIYLKAP-CTEPCGNSTCLVCPQDT-FLAMENHHNHCCARQCACDE-QAS 100

Db 114 EVEL-NCTRTQNTKCRCKPNEFCNSTVCEHC 143
: : : : : : : : : : : :
QY 101 QVALENCASAVADTRCGCKPGWFEVCQS-QC 130

RESULT 10
ENTRY GQVZML #type complete
TITLE T2 protein - myxoma virus (strain Lausanne)
ORGANISM #formal_name myxoma virus
DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

ACCESSIONS A40566
REFERENCE A40566
#authors Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
#journal Virology (1991) 184:370-382
#title Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence.

#cross-references MUID:91335768
#accession A40566
##molecule_type DNA
##residues 1-326 ##label UPT
##cross-references GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310

CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat homology

KEYWORDS glycoprotein

FEATURE 64-105 #domain NGF receptor repeat homology #label NG2\
106-147 #domain NGF receptor repeat homology #label NG3\
66,181,205,238 #binding_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 326 #molecular_weight 35208 #checksum 9255

Query Match 5.7%; Score 182; DB 1; Length 326;
Best Local Similarity 30.9%; Pred. No. 8.07e-13;
Matches 34; Conservative 23; Mismatches 45; Indels 8; Gaps 8;

Db 5 TILLAVACVYGGAGRYGADRGKRGNDYERKDL-CCTSCPPSYASRLCG-PSDVTYCS 62
14 ALLVLLGARAQGGTR-SP-KCDACADPFHKIGLFCRCRCPAGHYLKAPCTEPCGNSTCL 71
63 PCKNETFTT-STNHAPACVSCRGRTGHLSE-S-QSCDRTRDVPCDSAG 109
72 VCPQDTFLAMENHNHNECARCOA-CDEQASQVALENCASVADTRCGCKPG 120

RESULT 11
ENTRY D36858 #type complete
TITLE gene G4R protein - variola virus
ALTERNATE_NAMES B28R protein (COP)
ORGANISM #formal_name variola virus
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999

ACCESSIONS D36858; S46888; S32385; S35987
REFERENCE A36859
#authors Blinov, V.M.
#submission submitted to GenBank, November 1992
#description not shown.
#accession D36858
##status Preliminary
##molecule_type DNA
##residues 1-349 ##label BLI
##cross-references GB:X69198; NID:g456758; PID:g457087
##experimental_source strain India-1967, ssp. major, isolate Ind3 S46888

REFERENCE
#authors Koltyhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.V.; Tomenin, A.V.; Shchelkunov, S.N.; Sandakhchiev, L.S.
#submission submitted to the EMBL Data Library, April 1992
#description Nucleotide sequence analysis of the region of variola virus XhoI F O H P Q genome fragment.
#accession S46888
##status Preliminary
##molecule_type DNA
##residues 1-349 ##label KOL
##cross-references EMBL:X67117; NID:g516428; PID:g516449
##experimental_source strain India-1967, isolate Ind3

REFERENCE S32385
#authors Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
#journal FEBS Lett. (1993) 319:80-83
#title Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.
#cross-references MUID:93202281
#accession S32385
##molecule_type DNA
##residues 31-168 ##label SHC
##cross-references EMBL:X69198
##experimental_source strain India-1967, ssp. major

GENETICS

CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat homology

FEATURE 32-66 #domain NGF receptor repeat homology #label NGF\
68-109 #domain NGF receptor repeat homology #label NG2\
110-151 #domain NGF receptor repeat homology #label NG3

SUMMARY #length 349 #molecular_weight 38189 #checksum 2016

Query Match 5.6%; Score 179; DB 2; Length 349;
Best Local Similarity 27.1%; Pred. No. 2.56e-12;
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7;

Db 15 IIRGROAARYPTPNGCKDREY-KRNL-CCLSCPRTYASRLC-DSKTTQCTPCGSG 71
18 VLLCARAQGGTRSPDC-ACDFHKKIGLFCRCRCPAGHYLKAPCTEPCGNSTCLVCPD 76
72 TETSRNHL-PACLSCNGRCN-SNOYETRSCNTNHRICESPQY 115
77 TFLAMENHNHNECARCOA-CDEQASQVALENCASVADTRCGCKPGW 122

RESULT 12
ENTRY A46517 #type complete
TITLE CD27 antigen precursor - human
ALTERNATE_NAMES CD27L receptor; T cell activation antigen CD27
ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999

ACCESSIONS A46517; A46454
REFERENCE A46517
#authors Loenen, W.A.; Gravesteln, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.
#journal J. Immunol. (1992) 149:3937-3943
#title Genomic organization and chromosomal localization of the human CD27 gene.
#cross-references MUID:93094588
#accession A46517
##status not compared with conceptual translation
##molecule_type DNA
##residues 1-260 ##label LOE
##note sequence extracted from NCBI backbone (NCBI:P.120386)
##note authors propose an alternative repeat pattern

REFERENCE A46454
#authors Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
#journal J. Immunol. (1991) 147:3165-3169
#title The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor gene family.
#cross-references MUID:92013149
#accession A46454
##molecule_type RNA
##residues 1-58, 'A', 60-260 ##label CAM
##cross-references GB:M63928; NID:g180084; PIDN:AAA58411.1; PID:g180085
##note sequence extracted from NCBI backbone (NCBI:N.60285, NCBI:P.60289)

COMMENT A soluble CD27 found in serum and urine is formed by proteolysis.
GENETICS
#gene GDB:CD27
#cross-references GDB:132582; OMIM:186711
#map_position 12p13-12p13
#introns 46/71; 90/71; 150/71; 180/71; 220/71

```

CLASSIFICATION
KEYWORDS
FEATURES
    1-20 #domain signal sequence #status predicted #label SIG\
    21-260 #product CD27 antigen #status predicted #label MxV\
    21-191 #domain extracellular #status predicted #label EXT\
    27-63 #domain NGF receptor repeat homology #label NG1\
    65-105 #domain NGF receptor repeat homology #label NG2\
    121-188 #region proline/serine/threonine-rich\
    192-211 #domain transmembrane #status predicted #label TMN\
    212-260 #domain intracellular #status predicted #label INT\
    95 #binding_site carbohydrate (Asn) (covalent) #status
        predicted
SUMMARY
    #length 260 #molecular-weight 29186 #checksum 1652

Query Match 5.4%; Score 174; DB 1; Length 260;
Best Local Similarity 25.4%; Pred. No.1,73e-11;
Matches 31; Conservative 34; Mismatches 48; Indels 9; Gaps 7;

Db 9 LCVLGTLGLSLATPAPK--SCPERHWAGKLCCOMCEPTFLVKDCDOHNRKTACQPCIP 67
| : | : | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 17 LVLLDA-RAGGTGRSPRCACADPFHKIKLIFCRRGCPACHYLAKPTFCGNSTCLVC-P 74
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 GVSFSP-DHTTRPHCESCHCN--SGLL-VRNCTITANAECACRNGW--QCQRDKETED 121
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 75 QDTFLAENHHNSCARCOACDEASQVALENCSAVDATRCGCPCGMFECCGVSVCSVS 134
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 122 PL 123
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 135 PF 136

RESULT 13
ENTRY A35356 #type complete
TITLE tumor necrosis factor receptor type 2 precursor - human
ALTERNATE_NAMES 75K tumor necrosis factor receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
ACCESSIONS A35356; A36475; A48416; A36007; A23666; B35010; I38094
REFERENCE A35356
#authors Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann,
M.P.; Jerry, R.; Dowey, S.K.; Cosman, D.; Goodwin, R.G.
Science (1990) 248:1019-1023
#journal A receptor for tumor necrosis factor defines an unusual
#title family of cellular and viral proteins.
#cross-references MUID:90260639
#accession A35356
#status preliminary
#molecule_type mRNA
#residues 1-461 ##label SMT
#cross-references GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
A36475
REFERENCE A36475
#authors Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King,
M.W.; Hale, K.K.; Squires, C.H.; Thompson, R.C.; Vannice,
J.L. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8331-8335
#journal A second tumor necrosis factor receptor gene product can shed
#title a naturally occurring tumor necrosis factor inhibitor.
#cross-references MUID:91045991
#accession A36475
#status preliminary
#molecule_type mRNA
#residues 1-195; R', 197-461 ##label KOH
#cross-references GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1;
PID:g339758
REFERENCE A48416
#authors Dembic, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.;
Gertz, R.; Roetschhaus, M.; Lesstauer, W.
Cytokine (1990) 2:231-237
#journal Two human TNF receptors have similar extracellular, but
#title distinct intracellular, domain sequences.
```

```

#cross-references MUID:91370690
#accession A48416
#status preliminary
#molecule_type mRNA; protein
#residues 23-461 ##label DEM
#cross-references GB:S63366; NID:g235648; PIDN:AA819824.1; PID:g235649
##note sequence extracted from NCBI backbone (NCBIN:63368,
NCBP:63371)

REFERENCE
#authors Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang,
D.; Ringold, G.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
#title Complementary DNA cloning of a receptor for tumor necrosis
factor and demonstration of a shed form of the receptor.
#cross-references MUID:90349572
#accession A36007
#status preliminary
#molecule_type mRNA
#residues 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 ##label HEL
#cross-references GB:M35857; NID:g339751; PIDN:AA63262.1; PID:g339752
#accession A23666
#authors Loetscher, H.; Schlaefer, E.J.; Lahm, H.W.; Pan, Y.C.E.;
Lesslauer, W.; Brockhaus, M.
#journal J. Biol. Chem. (1990) 265:20131-20138
#title Purification and partial amino acid sequence analysis of two
distinct tumor necrosis factor receptors from HL60 cells.
#cross-references MUID:91056048
#accession A23666
#status preliminary
#molecule_type protein
#residues 23-40; 65-69; 136-141; 300-306 ##label LOE

REFERENCE
#authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession B35010
#status preliminary
#molecule_type protein
#residues 27-31 ##label ENG

REFERENCE
#authors Kuhnert, P.; Kemper, O.; Wallach, D.
#journal Gene (1994) 150:381-386
#title Cloning, sequencing and partial functional characterization
of the 5' region of the human p75 tumor necrosis factor
receptor-encoding gene (TNF-R).
#cross-references MUID:95121934
#accession I38094
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-37 ##label RES
#cross-references EMBL:X80021; NID:g666044; PIDN:CA56324.1;
PID:g825701

GENETICS
#gene GDB:TNFR2
#cross-references GDB:125914; OMIM:191191
#map_position 1p36.2-1p36.2
#introns 26/3
#note the list of introns is incomplete
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 2; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
#domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 2 #status
experimental #label MAT\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain Transmembrane #status predicted #label TM\

FEATURE
1-22
23-416
40-76
78-119
120-162
164-201
262-279

```

```

280-461      #domain intracellular #status predicted #label IMF\
171,193      #binding_site carbohydrate (Asn) (covalent) #status
              predicted
SUMMARY      #length 461 #molecular-weight 48291 #checksum 5724

Query Match      5.3%; Score 168; DB 1; Length 461;
Best Local Similarity 27.6%; Pred. No. 1,67e-10;
Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;

Db 44 EYDQTAQMCCSKSPGQAHVCTKT-SDTVCDSCEDSTYTOLM-NW-VPECLSGSRC 100
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 38 DFHKIKIGLFCCRCGPAGHYLKAPCTEPCGNSTGLVCPDTFFLA-WENHHNSECARQCA-C 95
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 101 S--SDQVETQACTREONRICTCRPGWT 125
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 96 DEQASQVALENCASAVADTRCGCKRPGWP 122

RESULT 14
ENTRY      S12783      #type complete
TITLE      OX40 antigen precursor - rat
ALTERNATE_NAMES
ORGANISM   nerve growth factor receptor homolog
            #format.name Rattus norvegicus #common.name Norway rat
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
            20-Sep-1999

ACCESSIONS
REFERENCE   S12783
#authors    Mallet, S.; Fossum, S.; Barclay, A.N.
#journal     EMBO J. (1990) 9:1063-1068
#title       Characterization of the MRC OX40 antigen of activated CD4
             positive T lymphocytes - a molecule related to nerve growth
             factor receptor.
             Factor receptor.
#cross-references MIMID:90214614
#accession   S12783
#molecule_type mRNA
#residues    1-271 ##label MAL
CLASSIFICATION
#cross-references EMBL:X17037; NID:g57830; PID:g57831
KEYWORDS     #superfamily CD27 antigen; NCR receptor repeat homology
             growth factor receptor; transmembrane protein
FEATURE
1-19         #domain signal sequence #status predicted #label SIG\
20-271       #product OX40 antigen #status predicted #label MAY\
211-225       #domain transmembrane #status predicted #label TM
#length 271 #molecular-weight 29895 #checksum 379

SUMMARY
Query Match      5.2%; Score 165; DB 2; Length 271;
Best Local Similarity 29.7%; Pred. No. 5,14e-10;
Matches 22; Conservative 17; Mismatches 32; Indels 3; Gaps 3;

Db 37 CCRECPGHGMVSR-C-DHTRDVYCHC-BEPGYN-EAVNYDTCKOCQCNHRSGSELKN 93
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 47 CCRGCPAGHYLKAPCTEPCGNSTGLVCPDTFFLA-WENHHNSECARQCADQASQVALEN 106
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 94 CMPTEDTVQCRRPG 107
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 107 CSAVADTRCGCKRPG 120

RESULT 15
ENTRY      B43692      #type complete
TITLE      T2 protein - rabbit fibroma virus
ORGANISM   #format.name rabbit fibroma virus, Shope fibroma virus
            30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
DATE       07-May-1999

ACCESSIONS
REFERENCE   B43692
#authors    Upton, C.; Delange, A.M.; McFadden, G.
#journal     Virology (1987) 160:20-30
#title       Tumorigenic poxviruses: genomic organization and DNA sequence
             of the telomeric region of the Shope fibroma virus genome.
#cross-references MIMID:87321103
#accession   B43692
#status      preliminary

```

FEATURE		CLASSIFICATION	
#molecule	type DNA	#residues	1-325
#cross-references	GB:M17433	#superfamily	myxoma virus T2 protein; NGF receptor repeat
64-105	#domain NGF receptor repeat	homology	homology
106-147	#domain NGF receptor repeat		
SUMMARY			
Query Match	5.1%	Score 164;	DB 2; Length 325;
Best Local	Similarity 33.0%;	Pred. No. 7,46e-10;	
Matches	29; Conservative 15;	Mismatches 36;	Indels 8; Gaps
Db	28 CGGHDYEND-GL-CCASCHPFGYASRLQG-PGSNTVSCPEDGTFTA-STNHAPACVSCR 83		
QY	35 CAG-DFHKIKILFCRCRGPAGHYLKPACTEPCGSGNSTGLVCPQDTFLAMENHHNSECARQ 93		
Db	84 GRPTGHTLSE-S-OPCDRTHDVCNCSNG 109		
QY	94 A-CDEQASQVALENCMSAVADTRCCQKPR 120		

Search completed: Tue Jul 25 22:24:41 2000
Job time : 25 secs.

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 W31517 (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 25 22:24:59 2000; Maspar time 13.86 Seconds
 Tabular output not generated. 712.501 Million cell updates/sec

Title: >US-09-314-889-4
 Description: (1-417) from US09314889.pap
 Perfect Score: 3198
 Sequence: 1 MEGRPRGCAVAAALLVL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table:
 PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 35.628; Variance 153.996; scale 0.231

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3198	100.0	417	1	W31517	6.61e-300
2	3198	100.0	417	1	W95538	6.61e-300
3	3198	100.0	417	1	W57045	6.61e-300
4	3198	100.0	417	1	W26709	6.61e-300
5	3198	100.0	417	1	W64486	6.61e-300
6	3118	97.5	428	1	W31516	6.01e-292
7	3118	97.5	428	1	W95537	6.01e-292
8	1962	61.4	411	1	W57046	2.99e-177
9	1422	44.5	181	1	W26708	5.28e-124
10	503	15.7	65	1	W93610	6.46e-35
11	412	12.9	909	1	W64485	2.15e-26
12	408	12.8	455	1	R07451	6.26e-26
13	407	12.7	455	1	R10986	6.26e-26
14	407	12.7	455	1	R75084	6.26e-26
15	407	12.7	455	1	R42059	6.26e-26
16	404	12.6	455	1	R11082	1.19e-25
17	404	12.6	455	1	R20787	1.19e-25
18	400	12.5	443	1	R51033	2.79e-25
19	400	12.5	455	1	R51034	2.79e-25
20	400	12.5	455	1	R42197	2.79e-25
21	364	12.3	455	1	R12550	1.00e-24
22	387	12.1	433	1	R51032	4.46e-24
23	372	11.6	455	1	R24000	1.08e-22

24	351	11.0	461	1	R07450	Rat Tumour Necrosis Fa	9.19e-21
25	273	8.5	256	1	W33357	TBP(20-161)/hCG-alpha	1.05e-13
26	248	7.8	307	1	W33358	TBP(20-161)/hCG-beta f	1.73e-11
27	250	7.8	336	1	W33360	TBP(20-190)/hCG-beta f	1.15e-11
28	245	7.7	108	1	W73570	Cytoplasmic domain of	3.17e-11
29	246	7.7	199	1	R24080	Truncated TNF-alpha 55	2.59e-11
30	246	7.7	211	1	W89225	Tumour necrosis factor	2.59e-11
31	247	7.7	285	1	W33359	TBP(20-190)/hCG-alpha	2.11e-11
32	246	7.7	309	1	R70108	TNF-R-GBP fusion prot	2.59e-11
33	246	7.7	311	1	W89229	Tumour necrosis factor	2.59e-11
34	246	7.7	366	1	W89228	Tumour necrosis factor	2.59e-11
35	246	7.7	371	1	R07449	Tumour Necrosis Factor	2.59e-11
36	246	7.7	397	1	W89227	Tumour necrosis factor	2.59e-11
37	246	7.7	417	1	W89226	Tumour necrosis factor	2.59e-11
38	246	7.7	420	1	W89224	Tumour necrosis factor	2.59e-11
39	246	7.7	451	1	R70107	TNF-R-GBP 130 fusion p	2.59e-11
40	246	7.7	547	1	R70104	TNF-R-GBP fusion prot	2.59e-11
41	246	7.7	900	1	R70103	TNF-R-GBP 130 fusion p	2.59e-11
42	246	7.7	1245	1	R70106	TNF-R-Pl. vivax Duffy	2.59e-11
43	246	7.7	1604	1	R70105	TNF-R-DBA 175 fusion p	2.59e-11
44	243	7.6	884	1	R70109	TNF-R-GBP 130 fusion p	4.75e-11
45	240	7.5	161	1	R27496	Native 30 kD TNF inhib	8.70e-11

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	W31517 standard; Protein; 417 AA.	
AC	W31517;	
DC	02-MAR-1998 (first entry)	
DE	Death domain containing receptor DR3.	
KW	Death domain containing receptor; DR3-VI; human; apoptosis; inflammation; NF-kappaB.	
OS	Homo sapiens.	
EH	Key	Location/Qualifiers
FT	Peptide	1..24
FT	Domain	/label= Sig-peptide
FT	Domain	25-201
FT	Domain	/note= "extracellular domain"
FT	Domain	202..224
FT	Domain	/note= "transmembrane domain"
FT	Domain	225..417
FT	Domain	/note= "intracellular domain"
FT	Domain	342..408
FT	Domain	/note= "death domain"
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	(UNMT) UNIV MICHIGAN.	
PD	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;	
PF	17-OCT-1996; U16849.	
PR	12-MAR-1996; US-013285.	
DR	WPI: 97-470812/43.	
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-VI -	
PT	for activation of apoptosis and NF-kappaB, antagonists can be used	
PS	Claim 1; Page 75-77; 108pp: English.	
CC	This protein comprises human death domain containing receptor	
CC	DR3, a novel member of the tumour necrosis factor receptor	
CC	family. Its amino acid sequence was deduced from a cDNA clone	
CC	(see T89427) isolated from a HUVEC cDNA library. Related death	
CC	domain containing receptor DR3-VI (see W31516) has also been	
CC	identified. Recombinant full-length or mature DR3, or the	
CC	extracellular, transmembrane, intracellular or death domain of	
CC	DR3 can be expressed in transformed host cells. These polypeptides	
CC	inhibition of apoptosis, or to screen for modulator compounds.	
CC	Antagonists, such as antibodies raised against DR3-VI, can be used	
CC	to treat diseases and disorders associated with increased apoptosis	
CC	and for treating inflammatory diseases and disorders.	
SQ	Sequence 417 AA;	

Query Match	100.0%	Score 3198:	DB 1:	Length 417:
Best Local Similarity 100.0%		Pred. No. 6,616-300:		
Matches 417: Conservative		0:	Mismatches 0:	Indels 0: Gaps 0:
Db 1	MEORRGCAAAVALLLVLLGARAAGGTGRSPRCACAGPFHKKIGLFFCCRGCPAGHYLKAP	60		
Qy 1	MEQRRGCAAAVALLLVLLGARAAGGTGRSPRCACAGPFHKKIGLFFCCRGCPAGHYLKAP	60		
Db 61	CTEPGCGNSTCLVCPDPTFLAENHHNSCACCQACDBQASVALAENSAAVADTFCGKRG	120		
Qy 61	CTEPGCGNSTCLVCPDPTFLAENHHNSCACCQACDBQASVALAENSAAVADTFCGKRG	120		
-Db 121	WEVEQVQCVSSSPFYQCPCLDCGALRRHRLCSRDDTCGTLPGFEHGDGCVCSP	180		
Qy 121	WEVEQVQCVSSSPFYQCPCLDCGALRRHRLCSRDDTCGTLPGFEHGDGCVCSP	180		
Db 181	TSTLGSCEPRCAVCGMROMFVOLLGLAVPLLLGATLTYTRHCPHKEPLVTADEAG	240		
Qy 181	TSTLGSCEPRCAVCGMROMFVOLLGLAVPLLLGATLTYTRHCPHKEPLVTADEAG	240		
Db 241	MEALPPRPATHTSLPDSAHHTLLAPDSESEKICTVOVNSNTPGYPTFOALACQVYMSW	300		
Qy 241	MEALPPRPATHTSLPDSAHHTLLAPDSESEKICTVOVNSNTPGYPTFOALACQVYMSW	300		
Db 301	DQLPSRALGPAAPLTLSPESPAGSPAMMLQCGPOLYDMDAVPARRMKEFVRTGLREAE	360		
Qy 301	DQLPSRALGPAAPLTLSPESPAGSPAMMLQCGPOLYDMDAVPARRMKEFVRTGLREAE	360		
Db 361	IEAVEVEIGRFDDQOYEMLKRRRQOQPGGLGAVYAALERMGLDCEVEDLSRRLDRGP	417		
Qy 361	IEAVEVEIGRFDDQOYEMLKRRRQOQPGGLGAVYAALERMGLDCEVEDLSRRLDRGP	417		

ID	WT	2	standard:	Protein:	417 AA.
AC	W95538;				
DT	25-MAR-1999	(first entry)			
DE	Death domain containing receptor polypeptide (DR3).				
KW	Death domain: receptor; DR3-V1; DR3; recombinant.				
OS	Homo sapiens.				
FN	Key	Location/Qualifiers			
FT	Peptide	1..24	/note="signal peptide"		
FT	Protein	25..417	/note="mature protein"		
PN	J11000170-A.				
PD	06-JAN-1999.				
PE	12-MAR-1997; 057503.				
PR	06-FEB-1997; US-037341.				
PR	12-MAR-1996; US-013285.				
PR	17-OCT-1996; US-028711.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
PA	(UNMI) UNIV MICHIGAN.				
DR	WPI: 99-124390/11.				
DR	N-PSDB: X00925.				
PT	New death domain containing receptor and recombinant vector -				
PT	optionally comprising leader sequence				
PS	Claim 1: Fig 3; 50pp; Japanese.				
CC	The invention provides nucleotide sequences encoding death domain				
CC	containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone				
CC	is contained in ATCC depositon No. 97456 and the DR3 cDNA clone is				
CC	contained in ATCC depositon No. 97757. Recombinant vectors comprising				
CC	the nucleic acid sequences and optionally the leader sequences are used				
CC	for the recombinant production of the proteins. The present sequence				
CC	represents the amino acid sequence of a death domain containing receptor				
CC	polypeptide (DR3).				
Sequence	417 AA;				
Query Match	100.0%;	Score 3198;	DB 1;	Length 417;	
Best local Similarity	100.0%;	Pred. No. 6,61e-300;			
Matches 417;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY	1	MEQRRGCAAAALLLVLLGARGAGSTRSRPRCDGADPHKIKGLGFCGCGPAGHYTKAR	60
Db	61	CTEPGNGSTCLVCPQDTFTLMEHHNHSECARCOACDBQASQVALENGCSVADTRGCKRFG	120
QY	61	CTEPGNGSTCLVCPQDTFTLMEHHNHSECARCOACDBQASQVALENGCSVADTRGCKRFG	120
Db	121	MFVEQVSQCSSESPFCQCPCLDGCALHRTRLICSRPDGCTCLPGFYEHGDDGVSCP	180
QY	121	MFVEQVSQCSSESPFCQCPCLDGCALHRTRLICSRPDGCTCLPGFYEHGDDGVSCP	180
Db	181	TSTLGSCPERCAALCGMRQMFQVOLLGVLVPLLGATLTYYTRHCPHFKPLVTADEAG	240
QY	181	TSTLGSCPERCAALCGMRQMFQVOLLGVLVPLLGATLTYYTRHCPHFKPLVTADEAG	240
Db	241	MEALTPPATLSPLDASHHTLAPPOSSEKICIVOLGNSWMPGYPEPDBALCPQYTWSM	300
QY	241	MEALTPPATLSPLDASHHTLAPPOSSEKICIVOLGNSWMPGYPEPDBALCPQYTWSM	300
Db	301	DQPSRALPGAAATLSPESPAGSPAMMLPGPQIVDVMDAVPARMKKEFVRTLTGREAE	360
QY	301	DQPSRALPGAAATLSPESPAGSPAMMLPGPQIVDVMDAVPARMKKEFVRTLTGREAE	360
Db	361	TEAVEVEIGRRDOOYEMLKRMRQOPAGICAGAYAALEHNGLDGCYEDLRSRLQSRP	417
QY	361	TEAVEVEIGRRDOOYEMLKRMRQOPAGICAGAYAALEHNGLDGCYEDLRSRLQSRP	417

ID	WT57045 standard; Protein: 417 AA.
AC	W57045: 20-AUG-1998 (first entry)
DE	Human apoptosis inducing receptor.
KM	Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW	Type I transmembrane protein; tumour cell death; autoimmune disease; therapy.
OS	Homo sapiens.
PN	W09B14565-A1.
PD	09-APR-1998.
PF	03-OCT-1997; U17876.
PR	04-OCT-1996; U5-044456.
PA	(IMMAY) IMMUNEX CORP.
PI	Perkins PA.
DR	WPI: 98-240077/21.
DR	N-PsDB: V28700.
PT	DNA encoding apoptosis inducing receptor - which is Type I transmembrane protein, useful for regulating cell death
PS	Claim 16: Page 28-30; 45pp; English.
CC	This sequence is the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases
CC	Sequence 417 AA;
SQ	Sequence 417 AA;
Query Match	100.0%; Score 3198; DB 1; Length 417;
Best Local Similarity	100.0%; Pred. No. 6,61e-300;
Matches 417; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MEORPFGCAVAALALLVLLGARAQGTBSRPRDCADDFHKKTGLFCCRCGPAGHYTKAP 60
Qy	1 MEORPFGCAVAALALLVLLGARAQGTBSRPRDCADDFHKKTGLFCCRCGPAGHYTKAP 60
Db	CFEPCCNSCTLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENSAAVADPTCGCKPG 120
Qy	61 CFEPCCNSCTLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENSAAVADPTCGCKPG 120
Db	121 WPEVCQVSDCVSSPFYCPQCLDGCALHRRTRLCSRRDTCGTCLDFEYEHGDCVSCP 180

QY 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGTLPGFYEHDGCVSCP 180
DB 181 TSTLGSCEPCAAVCGMRFWMVYVLLAGLVVPLLLGATLTYYTRHCPHPLVTADAG 240
QY 181 TSTLGSCEPCAAVCGMRFWMVYVLLAGLVVPLLLGATLTYYTRHCPHPLVTADAG 240
DB 241 MEALTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPETQFALCPQVYWSW 300
QY 241 MEALTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPETQFALCPQVYWSW 300
DB 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFVRTGLREAE 360
QY 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFVRTGLREAE 360
DB 361 IEAVEVEIGFRDQOYEMLKRMOQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
QY 361 IEAVEVEIGFRDQOYEMLKRMOQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 4
ID W64486 standard; Protein: 417 AA.
AC W64486;
DT 14-APR-1998 (first entry)
DE Human apoptosis protein Apo-3.
KW Apo-3; apoptosis; human; therapy.
OS Homo sapiens.
FH Key
FT Peptide
FT 1..24 Location/Qualifiers
FT /label= Sig_peptide
FT 25..198
FT Domain
FT /note= "extracellular domain"
FT 199..224
FT Domain
FT /note= "transmembrane domain"
FT 225..417
FT Domain
FT /note= "intracellular domain"
FT 338..417
FT Domain
FT /note= "death domain"
FT 67
FT Modified_site
FT /note= "N-glycosylated"
FT 106
FT Modified_site
FT /note= "N-glycosylated"
FT 106
PN WO9737020-A1.
PD 09-OCT-1997.
PE 31-MAR-1997; U05230.
PR 23-SEP-1996; US-710802.
PR 01-APR-1996; US-625328.
PA (GETH) GENENTECH INC.
PI Ashkenazi AJ;
DR WPI: 97-503105/46.
DR N-PSDB: T91180.
PT Polypeptide(s) Apo-3 and Apo-2L1 - useful for regulating apoptosis
PT in mammalian cells
PS Claim 19; Page 46-48; 70pp; English.
CC This novel polypeptide, designated Apo-3, is a protein that
CC stimulates or induces apoptotic activity in mammalian cells
CC purposes. Its amino acid sequence was deduced from a human foetal
CC heart cDNA clone (see T91180). The N-terminal 181 amino acids of
CC Apo-3 are identical to the sequence of another novel apoptosis
CC polypeptide, Apo-2L1 (see W6709). Also claimed are: polypeptides
CC comprising the extracellular or death domain of Apo-3; chimeric
CC molecules comprising Apo-3 fused to a heterologous amino acid
CC sequence; antibodies that bind to Apo-3 or its extracellular
CC domain; nucleic acids encoding the polypeptides, as well as
CC vectors and host cells; a non-human transgenic animal containing
CC cells that express nucleic acid encoding Apo-3; and a non-human
CC knockout animal containing cells having an altered Apo-3 gene.
CC Apo-3 can be used to induce apoptosis or NF-kappa-B (NF-KB) - or
CC JNK-mediated gene expression for therapeutic purposes. Apo-3-IgG
CC fusion proteins can be used to inhibit apoptosis or NF-kB
CC induction or JNK activation for therapeutic purposes, and can
CC be used as immunogens for anti-Apo-3 antibody production.
CC Apo-3 or Apo-2L1 can also be used as assay standards. The
CC animals can be used in drug screening and development.

SO Sequence 417 AA;
Query Match 100.0%; Score 3198; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 6,616-300;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MEORRGCAAAVAAALLVLLGARAGGTRSPRCOCAGPFHKKIGLFCRCGCPAGHYLKAP 60
QY 1 MEORRGCAAAVAAALLVLLGARAGGTRSPRCOCAGPFHKKIGLFCRCGCPAGHYLKAP 60
DB 61 CTEPGNSTCLVCPQDFTLAMEHHNSPCARCOACDEQASQVLENCASVADTRCGCKRG 120
QY 61 CTEPGNSTCLVCPQDFTLAMEHHNSPCARCOACDEQASQVLENCASVADTRCGCKRG 120
DB 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGTLPGFYEHDGCVSCP 180
QY 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGTLPGFYEHDGCVSCP 180
DB 181 TSTLGSCEPCAAVCGMRFWMVYVLLAGLVVPLLLGATLTYYTRHCPHPLVTADAG 240
QY 181 TSTLGSCEPCAAVCGMRFWMVYVLLAGLVVPLLLGATLTYYTRHCPHPLVTADAG 240
DB 241 MEALTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPETQFALCPQVYWSW 300
QY 241 MEALTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPETQFALCPQVYWSW 300
DB 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFVRTGLREAE 360
QY 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFVRTGLREAE 360
DB 361 IEAVEVEIGFRDQOYEMLKRMOQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
QY 361 IEAVEVEIGFRDQOYEMLKRMOQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 5
ID W64486 standard; Protein: 833 AA.
AC W64486;
DT 20-OCT-1998 (first entry)
DE Human DR3 protein.
KW Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; DR3;
KW infection; graft rejection; antagonist; inhibitor; diagnostic.
OS Homo sapiens.
PN WO9832856-A1.
PD 30-JUL-1998.
PE 27-JAN-1998; U01464.
PR 05-FEB-1997; US-037829.
PR 28-JAN-1997; US-035722.
PA (HUMA-) HUMAN GENOME SCI INC.
PI (UNMT) UNIV MICHIGAN.
DR Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;
DR WPI: 98-427952/36.
PT Nucleic acid encoding human death domain-containing receptor 4 -
PT useful for therapeutic modulation of apoptosis, in e.g. cancer and
PT autoimmune diseases
PS Disclosure; Fig 2; 92pp; English.
CC This sequence represents the human death domain containing receptor-3
CC DR3 which is used in a method resulting in the isolation of a human death
CC domain containing receptor 4, DR4. DR4 agonists are used to increase
CC apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in
CC cases of cancer, autoimmune disease, viral or other infections,
CC inflammation, graft vs. host disease, acute or chronic graft rejection.
CC Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of
CC acquired immune deficiency syndrome, neurodegenerative disease,
CC myelodysplastic syndrome, ischaemic injury, toxin-induced liver damage,
CC septic shock, cachexia and anorexia, also a wide range of inflammatory
CC conditions. DR4 of fragments of the protein are used diagnostically, e.g.
CC to detect mutant forms of DR4 (possibly associated with disease), for
CC isolating the DR4 gene or related sequences and for chromosomal mapping.
SQ Sequence 833 AA;

Query Match 100.0%; Score 3198; DB 1; Length 833;

Best Local Similarity 100.0%; Pred. No. 6,61e-300;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEORPRGCAVAALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
1 MEORPRGCAVAALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 1 MEORPRGCAVAALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 61 CTPECGSTLCVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPG 120
61 CTPECGSTLCVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPG 120
QY 61 CTPECGSTLCVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPG 120
Db 121 WFEVCQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIP 180
121 WFEVCQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIP 180
QY 121 WFEVCQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIP 180
Db 181 TSTLGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAG 240
181 TSTLGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAG 240
-QY 181 TSTLGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAG 240
Db 241 MEALTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSW 300
241 MEALTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSW 300
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSW 300
Db 301 DQPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREA 360
301 DQPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREA 360
QY 301 DQPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREA 360
Db 361 IEAVEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 417
361 IEAVEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 417
QY 361 IEAVEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 417

RESULT 6
ID W31516 standard; Protein; 428 AA.

AC W31516; (first entry)
DE Death domain containing receptor DR3-V1.
KW Inflammation; NF-kappaB.
OS Homo sapiens.
FH Key
FT Peptide
FT 1..35 Location/Qualifiers
FT 36..212 /label= "sig_peptide"
FT Domain
FT 213..235 /note= "extracellular domain"
FT Domain
FT 236..428 /note= "transmembrane domain"
FT Domain
FT 353..419 /note= "intracellular domain"
FT Domain
FT 1..22 /note= "death domain"
FT Region
FT 33..56 /note= "antigenic region (Claim 16)"
FT Region
FT 59..82 /note= "antigenic region (Claim 16)"
FT Region
FT 95..112 /note= "antigenic region (Claim 16)"
FT Region
FT 122..133 /note= "antigenic region (Claim 16)"
FT Region
FT 161..177 /note= "antigenic region (Claim 16)"
FT Region
FT 179..190 /note= "antigenic region (Claim 16)"
FT Region
FT 196..205 /note= "antigenic region (Claim 16)"
FT Region
FT /note= "antigenic region (Claim 16)"

PN W09733904-A1.
PD 18-SEP-1997.
PF 17-OCT-1996; U16849.
PR 12-MAR-1996; US-013285.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI-) UNIV MICHIGAN.

PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
DR WPI: 97-470812/43.
DR N-PSDB: T89426.
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
PS Claim 1; Page 71-73; 108pp; English.
CC This protein comprises human death domain containing receptor
CC DR3-V1, a novel member of the tumour necrosis factor receptor
CC family. Its amino acid sequence was deduced from a cDNA clone
CC (see T89426) isolated from a human testis tumour library. Related
CC death domain containing receptor DR3 (see W31517) has also been
CC identified. Recombinant full-length or mature DR3-V1 can be
CC expressed in transformed host cells. These polypeptides can be
CC used to treat diseases and disorders associated with the inhibition
CC of apoptosis, or to screen for modulator compounds. Antagonists,
CC such as antibodies raised against DR3-V1, can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.
SQ Sequence 428 AA;

Query Match 97.5%; Score 3118; DB 1; Length 428;
Best Local Similarity 98.3%; Pred. No. 6.01e-292;
Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 15 RGSAPAPVQALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74
15 RGSAPAPVQALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74
QY 4 RRGCAAAVAALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
Db 75 PCGNSTCLVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPGMFV 134
75 PCGNSTCLVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPGMFV 134
QY 64 PCGNSTCLVCPDPTFLAMENHNHNSCARQACDEASOVALENCASAVADTRCGCKPGMFV 123
Db 135 ECVQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIPST 194
135 ECVQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIPST 194
QY 124 ECVQYSSCVSSSPFYCOPCLDCGALHRRHRLTLCRRDTCGTLCPGYEHGDCVSCIPST 183
Db 195 LGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAGMEA 254
195 LGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAGMEA 254
QY 184 LGSCEPERCAAVCGMRQMWVOLLAGLVPLLLGATLTYTTRHCHPMPHYLTADAGMEA 243
Db 255 LTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSMDL 314
255 LTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSMDL 314
QY 244 LTPPPATHLSPDLSAHTLLAPDSEKICTYQVLGNSWTPGYPTQALCPQVTSMDL 303
Db 315 PSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREAIEIA 374
315 PSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREAIEIA 374
QY 304 PSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARMKKEFYVTLGLREAIEIA 363
Db 375 VEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 428
375 VEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 428
QY 364 VEVEIGRRDOQYEMLKRWROQOPAGLGAAYVAALERMGLDGCVEEDLSRLQGP 417

RESULT 7
ID W95537 standard; Protein; 428 AA.

AC W95537; (first entry)
DE Death domain containing receptor polypeptide (DR3-V1).
KW Death domain; receptor; DR3-V1; DR3; recombinant.
OS Homo sapiens.
FH Key
FT Peptide
FT 1..35 Location/Qualifiers
FT 36..428 /note= "signal peptide"
FT Protein
FT /note= "mature protein"

PN U11000170-A.
PD 06-JAN-1999.
PF 12-MAR-1997; 057503.
PR 06-FEB-1997; US-037341.
PR 12-MAR-1996; US-013285.
PR 17-OCT-1996; US-028711.
PA (HUMA-) HUMAN GENOME SCI INC.

PA (JNM1) INIV MICHIGAN.
DR WPI: 99-124390/11.
N-PSDS: X00924.
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 1: Fig 1, 2: 50pp: Japanese.
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97457. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are used
CC for the recombinant production of the proteins. The present sequence
CC represents the amino acid sequence of a death domain containing receptor
CC polypeptide (DR3-V1).
CC Sequence 428 AA;
SQ

Query Match	97.5%;	Score 3118;	DB 1;	Length 428;
Best Local Similarity	98.3%;	Pred. No. 6.01e-292;		
Matches 407;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

Db	15	RGSAAPRAQALLVLLVGARAGGSTRSPDCAGDEHFKITGLTSCRCSPAGHLLKAPCTE	74
OY	4	RPRCAAAVAAALLLVLLGARGGGSTRSPDCGADDFHKITGLTSCRCSPAGHLLKAPCTE	63
Db	75	PGCNSTCLVCPQDFTFLAMENHNHSECAACQACQEAQVAALENCSAAADTRCGCKPCEV	134
OY	64	PCGNSTCLVCPQDFTFLAMENHNHSECAACQACQEAQVAALENCSAAADTRCGCKPCEV	123
Db	135	ECQVSQCVSSSPFYQCPRLDGCALHRRHTRLTCSRDTDCGTCPLPGYEHMGDGCVCPTST	194
OY	124	ECQVSQCVSSSPFYQCPRLDGCALHRRHTRLTCSRDTDCGTCPLPGYEHMGDGCVCPTST	183
Db	195	LGSCPERRCAANCGRQMFVWQVLLAGLVPLVLLGATLTITTYTRHCRPHKPLVTVADEAGMEA	254
OY	184	LGSCPERRCAANCGRQMFVWQVLLAGLVPLVLLGATLTITTYTRHCRPHKPLVTVADEAGMEA	243
Db	255	LTPPRATHLSPLDSAHNLLIAPDQSESEKICVYQVLGNSTMGYPETQALCPQYTWMSMDL	314
OY	244	LTPPRATHLSPLDSAHNLLIAPDQSESEKICVYQVLGNSTMGYPETQALCPQYTWMSMDL	303
Db	315	PSRALGPAAPFTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAFTEA	374
OY	304	PSRALGPAAPFTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAFTEA	363
Db	375	VEVEIGRFRDQYEMLKRWRQDQDAGIGATYAALERMGDGCYEDLRSRLQDRP	428
OY	364	VEVEIGRFRDQYEMLKRWRQDQDAGIGATYAALERMGDGCYEDLRSRLQDRP	417

	RESULT	8
ID	W57046	standard; Protein; 411 AA.
AC	W57046;	
DT	20-AUG-1998	(first entry)
DE	Mouse apoptosis inducing receptor.	
KM	Apoptosis inducing receptor; AIR protein; mouse; cell death regulator;	
KW	Type I transmembrane protein; tumour cell death; autoimmune disease;	
KW	therapy.	
OS	Mus sp.	
PN	W09814565-A1.	
PD	09-APR-1998.	
PF	03-OCT-1997; U17876.	
PR	04-OCT-1996; US-044456.	
PA	(IMMV) IMMUNEX CORP.	
PI	Perkins PA;	
DR	WPI; 98-240077/21.	
DR	N-PSDB; V28701.	
PT	DNA encoding apoptosis inducing receptor - which is Type I	
PT	transmembrane protein, useful for regulating cell death	
PS	Claim 16; Page 33-35; 45pp; English.	
CC	This sequence is the mouse apoptosis inducing receptor (AIR) of the	
CC	invention. AIR is a Type I transmembrane protein, soluble forms of which	
CC	can be used to regulate cell death in a therapeutic setting. Soluble AIR	
CC	can also be used in vitro to block apoptosis or AIR-expressing cells, or	

CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as *in vitro*. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
50 Sequence 411 AA;

Query Match	61.48;	Score 1962;	DB 1;	Length 411;
Best Local Similarity	65.98;	Pred. No. 2.99e-177;		
Matches	267;	Conservative	61;	Mismatches 61; Indels 16; Gaps 9;

Db	21	LLLLGGGGGGM-SGRCCDASSGCKRYGPGRCRGPKGHYMKAPCAEPGSGNSTCLJPCP	79
Qy	15	LLVLVLGARAGGGTRSPPCDCAOGFHKKIGLFCRRGPAGIYLLAPCTEPGSGNSTCLVCP	74
Db	80	SDTEFLTRNNHKTCTCRRQYCVDEBALAVTLFENCSAKSDTHGCGSCGVCSTSTEPCKSS	139
Qy	75	QDTLEAMNNHNSCARQACDQASQVALLFENCSAVADTRCGCKRGMFVEQYSGCASSS	134
Db	140	PPSCVPCGATTPVH-EAD---TPR-----PCLPGFYLRGNDCTISCPTGSSVCCPKACTAV	190
Qy	135	PFYQCPCLDCCALHNRHTRILCSRRDPTDGCPTGLPFYEHGDGCVSCSPSTLGSCEPCAAY	194
Db	191	CGMKQMFVQYLL-G--VAFLFGLALICAYCR-WQPKAVYTAADTAETLTLASQTHLS	246
Qy	195	CGMKQMFVQYLLGLVLPVLLGLATLYTYRHCN-PIKPLVTAADAEAMEALTPPRAHLS	253
Db	247	ASDSAHNTLLAPPSSTGKICTVTVLVGNMNPGLSTQTEVCGASGAPMDLPNTLGTPL	306
Qy	254	PLDSAHNTLLAPPSSEKICT-VOLVGSMTPTGYETDEALCPQVTHSWMDLPSSALCPAA	312
Db	307	ASPLSPAPAGSPAAVLIQPGPOLYDVNDVADVAPARRMKFEFVTLGLREAEI5AVEVEICRFR	366
Qy	313	APTLSPESPAGSPAMMILOPGPOLYDVNDVADVAPARRMKFEFVTLGLREAEI5AVEVEIGFR	372
Db	367	DOQVEMLKRWROQOPAGIGATYALALEMGLGECADLRSLRQRP	411
Qy	373	DOQVEMLKRWROQOPAGIGATYALALEMGLGECADLRSLRQRP	417

RESULT	9	
ID	W26708	standard; Protein; 181 AA.
AC	W26708;	
DT	14-APR-1998	(first entry)
DE	Human apoptosis protein Apo-2Li.	
KW	Apo-2Li; apoptosis; Apo-2 ligand inhibitor; human; therapy.	
OS	Homo sapiens.	
EH	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label= Sig_peptide
FT	Modified_site	67
FT		/note= "N-glycosylated"
FT	Modified_site	106
FT		/note= "N-glycosylated"
PN	W09737020-A1.	
PD	09-OCT-1997.	
PF	31-MAR-1997;	U05230.
PR	23-SEP-1996;	US-710802.
PR	01-APR-1996;	US-625328.
PA	(GETT) GENENTECH INC.	
PI	Ashkenazi AJ:	
DR	WPI: 97-503105/46.	
DR	N-FSDS: T91179.	
PT	Polypeptide(s) Apo-3 and Apo-2Li - useful for regulating apoptosis	
PT	in mammalian cells	
PS	Claim 1; Page 43-44; 70pp. English.	
CC	This novel polypeptide, designated Apo-2 ligand inhibitor	
CC	(Apo-2Li), can be used to inhibit apoptosis for therapeutic	
CC	purposes.. Its amino acid sequence was deduced from a human thymus	
CC	cDNA clone (see T91179) and is identical to amino acid residues	
CC	1-181 of another novel apoptosis polypeptide, Apo-3 (see	
CC	W26709).	
CC	It may be a soluble, truncated of secreted form of Apo-3	
CC	lacking some extracellular sequence as well as the transmembrane	

Db 435 IEEL 439
QY 409 LRSRL 413

RESULT 12
ID R07451 standard; protein; 455 AA.
AC R07451;
DT 29-JAN-1991 (first entry)
DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KM Infectious disease; parasitic disease; cachexia;
OS autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.
PN Homo sapiens.
PP 333438-A.
PD 24-OCT-1990.
PE 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
DR WPI; 90-321987/43.
DR N-PSDB; Q06285.
PT DNA encoding TNF binding protein and TNF-receptor - used in
PT tumour treatment and to understand mechanism to TNF action
PS Disclosure: Fig 91(1-2); 51pp; German.
CC ratTNF-R8 (Q06284) was used to screen the HS9137 cDNA library.
CC lambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC construct a plasmid (pADTNF-R) expressing the product the same way
CC as pADTNF-BP (see Q06282). The expressed proteins are useful
CC prophylactically and therapeutically to control disorders which
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC respiratory distress syndrome etc., or side effects of treatment with
CC TNG-alpha). They can also be used as diagnostic reagents for
CC assaying TNF and in study of TNF-receptor interactions.
CC See also Q06282-Q06285.
SQ Sequence 455 AA:

Query Match 12.8%; Score 408; DB 1; Length 455;
Best Local Similarity 29.9%; Pred. No. 5.05e-26;
Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDSVCPQGXIIHPONNSICTCKHKGITLYLNDCCPGQDPTDCRECS 86
QY 19 LLGARAGGGRSPR-CDCA-GDF-HKRTGLFCRCGCPAGHYLAKPCTEPCGNSSTCLVCPQ 75
Db 87 GSFTASENHLR-HCLSCSKCRKEMQVEISSCTVDRDTCGCRKNOYRHYW-SENLFQC- 143
QY 76 DFLAMENHNHNSCARQACDEQASVALENCASAVADTRCGCKPQWFEQVSCVSSSP 135
Db 144 FNCISLCIN-GTVH---LSCQEKONTVC-TCHAGFLRENECVSCSNCKKSLECTKLCIP 197
QY 136 FYCQPCIDCGALHRTLRLLC-SRRDTCGTCLPGFEYHGDGCVSCPSTILG-SCPERC-A 192
Db 198 QIENVKGTEDSGTVLLP-LVIFFGCLLSLFLIGLMYRQRMKSKLYSIYCKSTPEKE 256
QY 193 AVCGWRQMF-W-VQYLLAGLV--PL-LLGATLT-YTYR-HCWPHK--PLVYADAE-GME 242
Db 257 GELEGTTKPLAPNPSFPTGFTPTLGFSPVSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 316
QY 243 A-LTPPATHTLSPLDS-AHTL-LAPDSSSEKICHTVOLGNS-WTPGYPETQALCPQVT- 297
Db 317 PYGADPILATALASDPIPNPLOKMEDSAHKPOSJTDTPATLYAVENVPLRKKEFVR 376
QY 298 -W-SMDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPO-LYDVMADAVAPRRMKKEFVR 352
Db 377 RLGLSDHEIDRLQNGRCLEAPQYSMLATWRRTTTPREATTLELLGRLVLRMDLGLCED 436
QY 353 TLGLREAEIEAVEVEIGR-FRDOQYEMLKRMROQP---AGLGAVYALERMGIDGVED 408
Db 437 IEEL 441

QY 409 LRSRL 413

RESULT 13
ID R10986 standard; protein; 455 AA.
AC R10986;
DT 13-MAY-1991 (first entry)
DE 30kD TNF inhibitor precursor.
KW Tumour necrosis factor; inhibitor.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cleavage_site 40..41
FT note=" cleavage gives active protein "
PN AU9058976-A.
PD 24-JAN-1991.
PE 16-JUL-1990; 058976.
PR 18-JUL-1989; US-381080.
PR 11-DEC-1989; US-450329.
PR 07-FEB-1990; US-479661.
PA (SYNE-) SYNERGEN INC.
DR WPI; 91-073847/11.
DR N-PSDB; Q10883.
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
PS Disclosure: Fig 21; 142pp; English.
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC from which the sequence was deduced was isolated from a cDNA
CC library prep. from RNA from U937 cells treated with PMA/PMA.
CC The whole gene can be inserted into expression vectors for prepn.
CC of TNF inhibitor for use in the treatment of inflammatory and
CC degenerative diseases. The active protein is claimed (Claim 8).
SQ See also R10984 and R11001.
Sequence 455 AA:

Query Match 12.7%; Score 407; DB 1; Length 455;
Best Local Similarity 29.9%; Pred. No. 6.26e-26;
Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDSVCPQGXIIHPONNSICTCKHKGITLYLNDCCPGQDPTDCRECS 86
QY 19 LLGARAGGGRSPR-CDCA-GDF-HKRTGLFCRCGCPAGHYLAKPCTEPCGNSSTCLVCPQ 75
Db 87 GSFTASENHLR-HCLSCSKCRKEMQVEISSCTVDRDTCGCRKNOYRHYW-SENLFQC- 143
QY 76 DFLAMENHNHNSCARQACDEQASVALENCASAVADTRCGCKPQWFEQVSCVSSSP 135
Db 144 FNCISLCIN-GTVH---LSCQEKONTVC-TCHAGFLRENECVSCSNCKKSLECTKLCIP 197
QY 136 FYCQPCIDCGALHRTLRLLC-SRRDTCGTCLPGFEYHGDGCVSCPSTILG-SCPERC-A 192
Db 198 QIENVKGTEDSGTVLLP-LVIFFGCLLSLFLIGLMYRQRMKSKLYSIYCKSTPEKE 256
QY 193 AVCGWRQMF-W-VQYLLAGLV--PL-LLGATLT-YTYR-HCWPHK--PLVYADAE-GME 242
Db 257 GELEGTTKPLAPNPSFPTGFTPTLGFSPVSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 316
QY 243 A-LTPPATHTLSPLDS-AHTL-LAPDSSSEKICHTVOLGNS-WTPGYPETQALCPQVT- 297
Db 317 PYGADPILATALASDPIPNPLOKMEDSAHKPOSJTDTPATLYAVENVPLRKKEFVR 376
QY 298 -W-SMDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPO-LYDVMADAVAPRRMKKEFVR 352
Db 377 RLGLSDHEIDRLQNGRCLEAPQYSMLATWRRTTTPREATTLELLGRLVLRMDLGLCED 436
QY 353 TLGLREAEIEAVEVEIGR-FRDOQYEMLKRMROQP---AGLGAVYALERMGIDGVED 408
Db 437 IEEL 441
QY 409 LRSRL 413
RESULT 14

CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causative
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft verses
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.
SQ Sequence 455 AA;

Query Match 12.7%; Score 407; DB 1; Length 455;

Best Local Similarity 29.9%; Pred. No. 6.26e-26;

Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

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Db 27 VIGLPHLDREKRDVCPQGYIHPONNSICTKCHKGYLNDPCPGQDTRCECES 86
QY 19 LIGARAQGGTRSPR-CDCA-GDF-HKKIGLFCRCGPACHYLA PCTEPGNGSTCLVCPQ 75
Db 87 GSFTASENHLR-HCLSCSKREKEMGOVEISSCTVDRDTVCGCRKNQRYHYW-SENLFQC- 143
QY 76 DFLAMENHNHNECARCQACDEQASQVALENCASAVADTRCGCKPGMFVEQVQSCVSSSP 135
Db 144 FMSCLCN-GTVH---LSCQEKQNTVC-TCHAGFLRENECVSGSNCKKSLECTKLCUP 197
QY 136 FYCQPCLDGALHRTLRILC-SRRTDCCGTCLPGEYEHGDCVSCPTSLG-SCPERC-A 192
Db 198 OLENYKGTEDSGTYLLP-LVTFPGICLISLFLIGLMRYQRMKSKLYSYCGSKSTPEKE 256
QY 193 AYCGRKQMF-W-VQVLLAGLV--PL-LIGATLT-YTYR-HCPHK--PLVTADCA-GME 242
Db 257 GELEGTTKPLAPNPSFSPPTGFTPLGFSVPSSSTFTSSSTYTPGDCPFNFAAPRRVAP 316
QY 243 A-LTPPPATHLSPLDS-AHTL-LAPDSSSEKICTVQVGNL-WTPGYETQEALCPQVT- 297
Db 317 PYGADPIATALASDPITPNLQKWEDESAHKPOSILDTDDPATLYAVENVPLRWKEFVR 376
QY 298 -W-SWDOLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPO-LYDVMDAVPARRWKEFVR 352
Db 377 RLGLSDHEIDRLONGRCLEAOYSMLATWRRRTPRREATLELGRVLBDMDLGLCLED 436
QY 353 TLGLREAELEAVEVEIGR-FRDOYEMLRKRWQOP--AGLGAVYALERMGLDGCVED 408
Db 437 IEAL 441
QY 409 IRSRL 413
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